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**Human Nucleic Acid Sequences from Endometrial Tumor Tissue**

The invention relates to human nucleic acid sequences from endometrial tumors, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer in women is the endometrial tumor, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

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A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer ( $> 2000$  nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this possibility of error can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, which play a role as candidate genes in endometrial tumors, have now been found.

Nucleic acid sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555,
  - b) an allelic variation of the nucleic acid sequences named under a)
- or
- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-126 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

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The invention also relates to nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, which are expressed elevated in the endometrial tumor.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs,  $\phi$ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia),
2. eukaryotic,

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The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides, according to the sequence protocols Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of ORF ID Nos. 142-528 and Seq. ID Nos. ORF 561-575, 577-625, and 630-635 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

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The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635 according to the invention can also be used as tools for finding active ingredients against endometrial tumors, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 for expression of polypeptides, which can be used as tools for finding active ingredients against endometrial tumors.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 142-528 and Seq. ID Nos. 561-575, 577-625, and 630-635 as pharmaceutical agents in the gene therapy for treatment of uterus tumors or for the production of a pharmaceutical agent for treatment of uterus tumors.

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The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-141 and Seq. ID Nos. 531-552, 554, and 555, genomic BAC, PAC and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq.

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ID Nos. 531-552, 554, and 555, for use as vehicles for gene transfer.

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## Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring amino acids

## Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

## Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

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- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

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The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

#### **Example 1**

##### **Search for Tumor-related Candidate Genes**

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

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Figures 2b1-2b4 illustrate the lengthening of the uterus tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

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**Example 2****Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

**2.1. Electronic Northern Blot**

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

**2.1.1**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 136 was found, which occurs 15.6 x more strongly in the endometrial tumor than in normal tissue.

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The result is as follows:

Electronic Northern for SEQ. ID NO.: 136

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0102	0.0038	2.7221	0.3674
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0090	0.0078	1.1513	0.8686
Endocrine tissue	0.0000	0.0150	0.0000	undef
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0059	0.0031	1.9199	0.5209
Hematopoietic	0.0040	0.0379	0.1059	9.4460
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0114	0.0041	2.7942	0.3579
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0103	0.0120	0.8567	1.1673
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0104			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	-0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0142	Skin-muscle	0.0000
Suprarenal gland	0.0108	Testicles	0.0164
Kidney	0.0254	Lung	0.0060
Placenta	0.0000	Nerves	0.0068
Prostate	0.0061	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
	0.0126	Uterus_n	

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In an analogous procedure, the following Northern were also found:

Electronic Northern for SEQ. ID NO.: 1				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0038	0.0056	0.6805	1.4694
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0104	0.2878	3.4745
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0030	0.0031	0.9599	1.0417
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0068	0.1055	0.0640	15.6211
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 2

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.3166	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development 0.0000  
Gastrointestinal 0.0000  
Brain 0.0000  
Hematopoietic 0.0000  
Skin 0.0000  
Hepatic 0.0000  
Heart-blood vessels 0.0000  
Lung 0.0000  
Suprarenal gland 0.0000  
Kidney 0.0000  
Placenta 0.0000  
Prostate 0.0000  
Sensory organs 0.0000

Breast 0.0000  
Ovary\_n 0.0000  
Ovary\_t 0.0000  
Endocrine tissue 0.0000  
Fetal 0.0122  
Gastrointestinal 0.0000  
Hematopoietic 0.0000  
Skin-muscle 0.0000  
Testicles 0.0000  
Lung 0.0000  
Nerves 0.0000  
Prostate 0.0000  
Sensory Organs 0.0000  
Uterus\_n

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Electronic Northern for SEQ. ID NO.: 3

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0078	0.0281	0.2774	3.6055
Small intestine	0.0090	0.0188	0.4764	2.0992
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0052	0.5756	1.7372
Gastrointestinal	0.0085	0.0176	0.4852	2.0611
Brain	0.0019	0.0093	0.2071	4.8289
Hematopoietic	0.0118	0.0123	0.9599	1.0417
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0058	0.0117	0.4920	2.0326
Stomach-esophagus	0.0073	0.0020	3.5562	0.2812
Muscle-skeleton	0.0097	0.0153	0.6303	1.5866
Kidney	0.0034	0.0240	0.1428	7.0040
Pancreas	0.0136	0.0274	0.4956	2.0176
Penis	0.0050	0.0000	undef	0.0000
Prostate	0.0090	0.0000	undef	0.0000
Uterus-endometrium	0.0109	0.0149	0.7312	1.3677
Uterus-myometrium	0.0068	0.1583	0.0427	23.4317
Uterus-general	0.0076	0.0272	0.2806	3.5642
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0160			
Seminal vesicle	0.0119			
Sensory organs	0.0178			
White blood cells	0.0000			
Cervix	0.0009			
	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0278	Breast	0.0272
Gastrointestinal	0.0194	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0203
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0114
Lung	0.0145	Skin-muscle	0.0194
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0124	Lung	0.0164
Placenta	0.0121	Nerves	0.0120
Prostate	0.0249	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0083

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Electronic Northern for SEQ. ID NO.: 4

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0000	undef	0.0000
Small intestine	0.0026	0.0000	undef	0.0000
Ovary	0.0000	0.0165	0.0000	undef
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0017	0.0000	undef	0.0000
Brain	0.0077	0.0000	undef	0.0000
Hematopoietic	0.0015	0.0021	0.7200	1.3890
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0011	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0021	0.0020	1.0161	0.9842
Muscle-skeleton	0.0193	0.0077	2.5211	0.3967
Kidney	0.0000	0.0060	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0076	0.0068	1.1223	0.8911
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0167

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Electronic Northern for SEQ. ID NO.: 5

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0026	1.5254	0.6555
Small intestine	0.0038	0.0038	1.0208	0.9796
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0060	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0093	0.0000	undef
Hematopoietic	0.0015	0.0021	0.7200	1.3890
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0053	0.0137	0.3855	2.5941
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0193	0.0000	undef	0.0000
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0017	0.0055	0.2991	3.3428
Prostate	0.0060	0.0267	0.2246	4.4517
Uterus-endometrium	0.0065	0.0021	3.0709	0.3256
Uterus-myometrium	0.0135	0.1055	0.1280	7.8106
Uterus-general	0.0000	0.0068	0.0000	undef
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0000			
Sensory organs	0.0178			
White blood cells	0.0000			
Cervix	0.0078			
	0.0000			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development 0.0000  
 Gastrointestinal 0.0083  
 Brain 0.0000  
 Hematopoietic 0.0079  
 Skin 0.0000  
 Hepatic 0.0000  
 Heart-blood vessels 0.0000  
 Lung 0.0036  
 Suprarenal gland 0.0000  
 Kidney 0.0000  
 Placenta 0.0000  
 Prostate 0.0000  
 Sensory organs 0.0000

Breast 0.0000  
 Ovary\_n 0.0000  
 Ovary\_t 0.0759  
 Endocrine tissue 0.0000  
 Fetal 0.0029  
 Gastrointestinal 0.0122  
 Hematopoietic 0.0057  
 Skin-muscle 0.0000  
 Testicles 0.0000  
 Lung 0.0040  
 Nerves 0.0000  
 Prostate 0.0000  
 Sensory Organs 0.0083  
 Uterus\_n

00673395 122700



Electronic Northern for SEQ. ID NO.: 6

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0077	2.0339	0.4917
Breast	0.0051	0.0075	0.6805	1.4694
Small intestine	0.0123	0.0331	0.3707	2.6973
Ovary	0.0120	0.0104	1.1513	0.8686
Endocrine tissue	0.0085	0.0075	1.1321	0.8833
Gastrointestinal	0.0096	0.0278	0.3451	2.8974
Brain	0.0133	0.0164	0.8100	1.2346
Hematopoietic	0.0120	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0170	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0197	0.0164	1.2066	0.8288
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0034	0.0180	0.1904	5.2530
Kidney	0.0054	0.0274	0.1983	5.0439
Pancreas	0.0066	0.0055	1.1966	0.8357
Penis	0.0240	0.0267	0.8985	1.1129
Prostate	0.0044	0.0192	0.2275	4.3961
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0229	0.0272	0.8417	1.1881
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0104			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0136
Gastrointestinal	0.0250	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0354
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0245
Hepatic	0.0260	Gastrointestinal	0.0244
Heart-blood vessels	0.0178	Hematopoietic	0.0228
Lung	0.0036	Skin-muscle	0.0551
Suprarenal gland	0.0000	Testicles	0.0386
Kidney	0.0000	Lung	0.0082
Placenta	0.0121	Nerves	0.0181
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0167

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Electronic Northern for SEQ. ID NO.: 7

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast				
Small intestine	0.0000	0.0000	undef undef	
Ovary	0.0026	0.0019	1.3611 0.7347	
Endocrine tissue	0.0061	0.0000	undef 0.0000	
Gastrointestinal	0.0060	0.0026	2.3025 0.4343	
Brain	0.0051	0.0000	undef 0.0000	
Hematopoietic	0.0096	0.0139	0.6903 1.4487	
Skin	0.0037	0.0092	0.4000 2.5001	
Hepatic	0.0013	0.0000	undef 0.0000	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0000	0.0000	undef undef	
Lung	0.0042	0.0000	undef 0.0000	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0042	0.0041	1.0161 0.9842	
Kidney	0.0097	0.0153	0.6303 1.5866	
Pancreas	0.0000	0.0120	0.0000 undef	
Penis	0.0027	0.0000	undef 0.0000	
Prostate	0.0017	0.0000	undef 0.0000	
Uterus-endometrium	0.0150	0.0000	undef 0.0000	
Uterus-myometrium	0.0087	0.0043	2.0473 0.4885	
Uterus-general	0.0068	0.1055	0.0640 15.6211	
Breast hyperplasia	0.0076	0.0000	undef 0.0000	
Prostate hyperplasia	0.0000	0.0000	undef undef	
Seminal vesicle	0.0032			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0097
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0155
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 8

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0000	0.0021	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 9

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED	
		% frequency	LIBRARIES	
			% frequency	
Development			Breast	0.0000
Gastrointestinal	0.0000		Ovary_n	0.0000
Brain	0.0000		Ovary_t	0.0000
Hematopoietic	0.0000		Endocrine tissue	0.0000
Skin	0.0000		Fetal	0.0006
Hepatic	0.0000		Gastrointestinal	0.0000
Heart-blood vessels	0.0000		Hematopoietic	0.0000
Lung	0.0000		Skin-muscle	0.0000
Suprarenal gland	0.0000		Testicles	0.0000
Kidney	0.0000		Lung	0.0000
Placenta	0.0000		Nerves	0.0000
Prostate	0.0000		Prostate	0.0000
Sensory organs	0.0000		Sensory Organs	0.0000
			Uterus_n	

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Electronic Northern for SEQ. ID NO.: 10

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

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## Electronic Northern for SEQ. ID NO.: 11

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0090	0.0188	0.4764	2.0992
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0050	1.0189	0.9815
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0066	0.0055	1.1966	0.8357
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0131	0.0213	0.6142	1.6282
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0178			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0106			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0154
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0342
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 12

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 13

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0038	0.0019	2.0416	0.4898
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0208	0.0000	undef
Gastrointestinal	0.0034	0.0201	0.1698	5.8889
Brain	0.0057	0.0000	undef	0.0000
Hematopoietic	0.0081	0.0072	1.1314	0.8839
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0010	0.0020	0.5080	1.9684
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0051	0.0000	undef	0.0000
Pancreas	0.0054	0.0000	undef	0.0000
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0065	0.0043	1.5354	0.6513
Uterus-myometrium	0.0068	0.1583	0.0427	23.4317
Uterus-general	0.0152	0.0000	undef	0.0000
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0149			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0309
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0100
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0250

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Electronic Northern for SEQ. ID NO.: 14

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency	% frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 15

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000		
Prostate hyperplasia	0.0000	0.0000		
Seminal vesicle	0.0000	0.0000		
Sensory organs	0.0000	0.0000		
White blood cells	0.0000	0.0000		
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development 0.0000  
Gastrointestinal 0.0000  
Brain 0.0000  
Hematopoietic 0.0000  
Skin 0.0000  
Hepatic 0.0000  
Heart-blood vessels 0.0000  
Lung 0.0000  
Suprarenal gland 0.0000  
Kidney 0.0000  
Placenta 0.0000  
Prostate 0.0000  
Sensory organs 0.0000

Breast 0.0000  
Ovary\_n 0.0000  
Ovary\_t 0.0000  
Endocrine tissue 0.0000  
Fetal 0.0000  
Gastrointestinal 0.0000  
Hematopoietic 0.0000  
Skin-muscle 0.0000  
Testicles 0.0000  
Lung 0.0000  
Nerves 0.0000  
Prostate 0.0000  
Sensory Organs 0.0000  
Uterus\_n

002227 5652960

Electronic Northern for SEQ. ID NO.: 16

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0153	0.0188	0.8166	1.2245
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0090	0.0182	0.4934	2.0268
Endocrine tissue	0.0187	0.0100	1.8679	0.5354
Gastrointestinal	0.0192	0.0324	0.5917	1.6901
Brain	0.0067	0.0205	0.3240	3.0866
Hematopoietic	0.0147	0.0379	0.3882	2.5762
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0143	0.0323	0.4412	2.2666
Heart	0.0148	0.0275	0.5397	1.8529
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0156	0.0102	1.5241	0.6561
Stomach-esophagus	0.0290	0.0307	0.9454	1.0578
Muscle-skeleton	0.0154	0.0120	1.2850	0.7782
Kidney	0.0407	0.0068	5.9478	0.1681
Pancreas	0.0132	0.0110	1.1966	0.8357
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0153	0.0085	1.7913	0.5582
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0229	0.0068	3.3668	0.2970
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0178			
Sensory organs	0.0353			
White blood cells	0.0165			
Cervix	0.0319			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development  
Gastrointestinal  
Brain  
Hematopoietic  
Skin  
Hepatic  
Heart-blood vessels  
Lung  
Suprarenal gland  
Kidney  
Placenta  
Prostate  
Sensory organs

0.0278  
0.0056  
0.0000  
0.0393  
0.0000  
0.0000  
0.0000  
0.0072  
0.0000  
0.0124  
0.0061  
0.0249  
0.0000

Breast  
Ovary\_n  
Ovary\_t  
Endocrine tissue  
Fetal  
Gastrointestinal  
Hematopoietic  
Skin-muscle  
Testicles  
Lung  
Nerves  
Prostate  
Sensory Organs  
Uterus\_n

0.0476  
0.0000  
0.1114  
0.0245  
0.0175  
0.0244  
0.0114  
0.0292  
0.0000  
0.0082  
0.0020  
0.0000  
0.0310  
0.0167

00673395 122700

Electronic Northern for SEQ. ID NO.: 17

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0051	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0111	0.0031	3.5998	0.2778
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0100
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0208
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 18

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0078	0.0256	0.3051	3.2777
Small intestine	0.0090	0.0113	0.7939	1.2595
Ovary	0.0092	0.0000	undef	0.0000
Endocrine tissue	0.0090	0.0286	0.3140	3.1849
Gastrointestinal	0.0255	0.0050	5.0944	0.1963
Brain	0.0096	0.0185	0.5177	1.9316
Hematopoietic	0.0044	0.0082	0.5400	1.8520
Skin	0.0134	0.0379	0.3529	2.8338
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0285	0.0194	1.4706	0.6800
Testicles	0.0042	0.0275	0.1542	6.4853
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0083	0.0184	0.4516	2.2144
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0060	0.0000	undef
Pancreas	0.0109	0.0274	0.3965	2.5219
Penis	0.0017	0.0110	0.1496	6.6857
Prostate	0.0060	0.0533	0.1123	8.9035
Uterus-endometrium	0.0262	0.0192	1.3648	0.7327
Uterus-myometrium	0.0068	0.1583	0.0427	23.4317
Uterus-general	0.0000	0.0068	0.0000	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0128			
Seminal vesicle	0.0297			
Sensory organs	0.0356			
White blood cells	0.0000			
Cervix	0.0113			
	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0152
Hematopoietic	0.0188	Endocrine tissue	0.0245
Skin	0.0039	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0107	Skin-muscle	0.0389
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0124	Nerves	0.0080
Prostate	0.0182	Prostate	0.0274
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0126	Uterus_n	0.0458

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## Electronic Northern for SEQ. ID NO.: 19

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0195	0.0102	1.9068	0.5244
Small intestine	0.0115	0.0132	0.8750	1.1429
Ovary	0.0123	0.0165	0.7415	1.3487
Endocrine tissue	0.0060	0.0078	0.7675	1.3029
Gastrointestinal	0.0119	0.0125	0.9509	1.0516
Brain	0.0096	0.0139	0.6903	1.4487
Hematopoietic	0.0096	0.0041	2.3399	0.4274
Skin	0.0080	0.0379	0.2117	4.7230
Hepatic	0.0330	0.2542	0.1300	7.6946
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0127	0.0000	undef	0.0000
Lung	0.0115	0.0468	0.2460	4.0652
Stomach-esophagus	0.0052	0.0082	0.6350	1.5747
Muscle-skeleton	0.0000	0.0153	0.0000	undef
Kidney	0.0086	0.0060	1.4278	0.7004
Pancreas	0.0081	0.0000	undef	0.0000
Penis	0.0050	0.0055	0.8974	1.1143
Prostate	0.0150	0.0267	0.5616	1.7807
Uterus-endometrium	0.0087	0.0106	0.8189	1.2211
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0458	0.0000	undef	0.0000
Prostate hyperplasia	0.0384			
Seminal vesicle	0.0030			
Sensory organs	0.0000			
White blood cells	0.0353			
Cervix	0.0113			
	0.0000			

FETUS  
% frequency

Development	0.0139
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0136
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0077
Lung	0.0000
Nerves	0.0040
Prostate	0.0000
Sensory Organs	0.0077
Uterus_n	0.0000

000221-56664950

Electronic Northern for SEQ. ID NO.: 20

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.2111	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395-122700

Electronic Northern for SEQ. ID NO.: 21

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395-122700



	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0128	0.0000 undef	
Breast	0.0051	0.0075	0.6805 1.4694	
Small intestine	0.0123	0.0000	undef 0.0000	
Ovary	0.0060	0.0104	0.5756 1.7372	
Endocrine tissue	0.0102	0.0125	0.8151 1.2268	
Gastrointestinal	0.0172	0.0093	1.8638 0.5365	
Brain	0.0052	0.0010	5.0397 0.1984	
Hematopoietic	0.0027	0.0000	undef 0.0000	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0065	0.0000 undef	
Heart	0.0201	0.0412	0.4883 2.0480	
Testicles	0.0288	0.0234	1.2299 0.8130	
Lung	0.0114	0.0184	0.6209 1.6105	
Stomach-esophagus	0.0097	0.0077	1.2605 0.7933	
Muscle-skeleton	0.0086	0.0180	0.4759 2.1012	
Kidney	0.0217	0.0000	undef 0.0000	
Pancreas	0.0149	0.0221	0.6731 1.4857	
Penis	0.0150	0.0000	undef 0.0000	
Prostate	0.0065	0.0170	0.3839 2.6051	
Uterus-endometrium	0.0000	0.1055	0.0000 undef	
Uterus-myometrium	0.0000	0.0068	0.0000 undef	
Uterus-general	0.0192	0.0000	undef undef	
Breast hyperplasia	0.0149			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0130			
White blood cells	0.0000			
cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0071	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0227
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0061	Nerves	0.0030
Prostate	0.0249	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0125

Electronic Northern for SEQ. ID NO.: 23

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0026	3.0509	0.3278
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0041	0.1800	5.5559
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0137	0.2313	4.3235
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0205	0.0000	undef
Pancreas	0.0066	0.0055	1.1966	0.8357
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0106			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0154
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0030
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 24

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0077	0.0000	undef
Small intestine	0.0064	0.0019	3.4026	0.2939
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0068	0.0025	2.7170	0.3681
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0118	0.0031	3.8398	0.2604
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0020	0.5080	1.9684
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0109	0.0000	undef	0.0000
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0044	0.0085	0.5118	1.9538
Uterus-myometrium	0.0000	0.1583	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0136
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0111
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0080
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0377	Sensory Organs	0.0000
		Uterus_n	0.0000

004221 5664960

Electronic Northern for SEQ. ID NO.: 25

	NORMAL	TUMOR	Ratios		
	% frequency	% frequency	N/T	T/N	
Bladder					
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0064	0.0000	undef	0.0000	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0030	0.0026	1.1513	0.8686	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0019	0.0000	undef	0.0000	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0110	0.0000	undef	0.0000	
Heart	0.0048	0.0000	undef	0.0000	
Testicles	0.0042	0.0000	undef	0.0000	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0041	0.0000	undef	
Muscle-skeleton	0.0097	0.0000	undef	0.0000	
Kidney	0.0051	0.0000	undef	0.0000	
Pancreas	0.0027	0.0000	undef	0.0000	
Penis	0.0017	0.0000	undef	0.0000	
Prostate	0.0030	0.0000	undef	0.0000	
Uterus-endometrium	0.0022	0.0000	undef	0.0000	
Uterus-myometrium	0.0000	0.1055	0.0000	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000	0.0000	undef	undef	
Prostate hyperplasia	0.0064				
Seminal vesicle	0.0000				
Sensory organs	0.0089				
White blood cells	0.0000				
Cervix	0.0000				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 26

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0038	0.0185	0.2071	4.8289
Brain	0.0037	0.0031	1.1999	0.8334
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0062	0.0041	1.5241	0.6561
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0136	0.0068	1.9826	0.5044
Pancreas	0.0000	0.0110	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0954	0.1067	9.3678
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0026			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0140
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0680
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0070
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 27

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0000	0.0125	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0059	0.0041	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0204
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0064
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0000
Nerves	0.0020
Prostate	0.0000
Sensory Organs	0.0232
Uterus_n	0.0083

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Electronic Northern for SEQ. ID NO.: 28

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0051	0.0000	undef
Small intestine	0.0153	0.0094	1.6333	0.6123
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0130	0.2303	4.3431
Gastrointestinal	0.0034	0.0025	1.3585	0.7361
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0030	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0184	0.0000	undef	0.0000
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0020	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0086	0.0060	1.4278	0.7004
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0033	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0256			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0204
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0105
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0520	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0060
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0167
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 29

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0128	0.0000	undef
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0078	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0038	0.0046	0.8283	1.2072
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0061	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0085	0.2559	3.9077
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0096	0.0000	undef	undef
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 30

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0104	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0167

00673395 "122700

Electronic Northern for SEQ. ID NO.: 31

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0026	1.5254	0.6555
Small intestine	0.0013	0.0056	0.2268	4.4083
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0078	0.0000	undef
Gastrointestinal	0.0017	0.0050	0.3396	2.9444
Brain	0.0038	0.0046	0.8283	1.2072
Hematopoietic	0.0037	0.0041	0.8999	1.1112
Skin	0.0067	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0042	0.0041	1.0161	0.9842
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0034	0.0060	0.5711	1.7510
Pancreas	0.0027	0.0137	0.1983	5.0439
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0000	0.0267	0.0000	undef
Uterus-endometrium	0.0022	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0076	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0224			
Seminal vesicle	0.0030			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0035			
	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0182
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0077
Lung	0.0082
Nerves	0.0010
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 32

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef undef	
Small intestine	0.0000	0.0038	0.0000 undef	
Ovary	0.0031	0.0000	undef 0.0000	
Endocrine tissue	0.0000	0.0000	undef undef	
Gastrointestinal	0.0068	0.0050	1.3585 0.7361	
Brain	0.0038	0.0000	undef 0.0000	
Hematopoietic	0.0022	0.0041	0.5400 1.8520	
Skin	0.0027	0.0000	undef 0.0000	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0048	0.0129	0.3676 2.7200	
Testicles	0.0032	0.0000	undef 0.0000	
Lung	0.0000	0.0000	undef undef	
Stomach-esophagus	0.0000	0.0020	0.0000 undef	
Muscle-skeleton	0.0000	0.0000	undef undef	
Kidney	0.0000	0.0000	undef undef	
Pancreas	0.0054	0.0000	undef 0.0000	
Penis	0.0000	0.0110	0.0000 undef	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0022	0.0043	0.5118 1.9538	
Uterus-myometrium	0.0068	0.1055	0.0640 15.6211	
Uterus-general	0.0000	0.0000	undef undef	
Breast hyperplasia	0.0000	0.0000	undef undef	
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0020
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00227 5667960

Electronic Northern for SEQ. ID NO.: 33

	NORMAL % frequency	TUMOR % frequency	Ratios N/T      T/N	
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.2639	0.0256	39.0528
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 34

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0010	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 35

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0026	0.0038	0.6805	1.4694
Ovary	0.0000	0.0165	0.0000	undef
Endocrine tissue	0.0000	0.0026	0.0000	undef
Gastrointestinal	0.0034	0.0000	undef	0.0000
Brain	0.0057	0.0000	undef	0.0000
Hematopoietic	0.0007	0.0021	0.3600	2.7779
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0032	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0082	0.1270	7.8735
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0034	0.0000	undef	0.0000
Pancreas	0.0081	0.0479	0.1699	5.8845
Penis	0.0000	0.0000	undef	undef
Prostate	0.0060	0.0000	undef	0.0000
Uterus-endometrium	0.0044	0.0021	2.0473	0.4885
Uterus-myometrium	0.0068	0.2639	0.0256	39.0528
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0052			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0340
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0029
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0171
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0246
Prostate	0.0000	Prostate	0.0030
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

00673395-12200

Electronic Northern for SEQ. ID NO.: 36

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0038	0.0019	2.0416	0.4898
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0034	0.0000	undef	0.0000
Brain	0.0057	0.0000	undef	0.0000
Hematopoietic	0.0015	0.0010	1.4399	0.6945
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0129	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395-122700

Electronic Northern for SEQ. ID NO.: 37

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

004227" 5622960



Electronic Northern for SEQ. ID NO.: 38

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0120	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0000

002221"56E2960

Electronic Northern for SEQ. ID NO.: 39

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0404	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0020	3.5562	0.2812
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0269	0.1066	0.2527	3.9571
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0101
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

002221" 5652960

Electronic Northern for SEQ. ID NO.: 40

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0030	0.0156	0.1919	5.2117
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0096	0.0231	0.4142	2.4145
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0083	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0106	0.2047	4.8846
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development 0.0139  
Gastrointestinal 0.0000  
Brain 0.0000  
Hematopoietic 0.0000  
Skin 0.0000  
Hepatic 0.0000  
Heart-blood vessels 0.0000  
Lung 0.0072  
Suprarenal gland 0.0000  
Kidney 0.0000  
Placenta 0.0000  
Prostate 0.0000  
Sensory organs 0.0000

Breast 0.0000  
Ovary\_n 0.0000  
Ovary\_t 0.0000  
Endocrine tissue 0.0047  
Fetal 0.0000  
Gastrointestinal 0.0000  
Hematopoietic 0.0000  
Skin-muscle 0.0000  
Testicles 0.0082  
Lung 0.0000  
Nerves 0.0000  
Prostate 0.0000  
Sensory Organs 0.0000  
Uterus\_n

00673395 122700

## Electronic Northern for SEQ. ID NO.: 41

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0057
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

0067395-122700

Electronic Northern for SEQ. ID NO.: 42

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0077	2.0339	0.4917
Breast	0.0051	0.0113	0.4537	2.2042
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0136	0.0251	0.5434	1.8403
Gastrointestinal	0.0153	0.0185	0.8283	1.2072
Brain	0.0118	0.0041	2.8798	0.3472
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0129	0.7353	1.3600
Heart	0.0064	0.0275	0.2313	4.3235
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0187	0.0164	1.1431	0.8748
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0081	0.0205	0.3965	2.5219
Pancreas	0.0182	0.0055	3.2906	0.3039
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0131	0.0213	0.6142	1.6282
Uterus-endometrium	0.0135	0.1583	0.0854	11.7158
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0199			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0204
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0399
Lung	0.0072	Skin-muscle	0.0454
Suprarenal gland	0.0000	Testicles	0.0231
Kidney	0.0000	Lung	0.0082
Placenta	0.0182	Nerves	0.0301
Prostate	0.0499	Prostate	0.0068
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0167

00673395-122700

Electronic Northern for SEQ. ID NO.: 43

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0117	0.0102	1.1441	0.8741
Small intestine	0.0102	0.0226	0.4537	2.2042
Ovary	0.0123	0.0165	0.7415	1.3487
Endocrine tissue	0.0030	0.0078	0.3838	2.6058
Gastrointestinal	0.0136	0.0150	0.9057	1.1042
Brain	0.0153	0.0046	3.3134	0.3018
Hematopoietic	0.0074	0.0103	0.7200	1.3890
Skin	0.0053	0.0379	0.1412	7.0845
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0143	0.0129	1.1029	0.9067
Testicles	0.0074	0.0137	0.5397	1.8529
Lung	0.0173	0.0000	undef	0.0000
Stomach-esophagus	0.0125	0.0164	0.7621	1.3122
Muscle-skeleton	0.0097	0.0153	0.6303	1.5866
Kidney	0.0154	0.0060	2.5700	0.3891
Pancreas	0.0109	0.0137	0.7930	1.2610
Penis	0.0083	0.0276	0.2991	3.3428
Prostate	0.0150	0.0533	0.2808	3.5614
Uterus-endometrium	0.0196	0.0149	1.3161	0.7598
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0000	0.0136	0.0000	undef
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0208			
Sensory organs	0.0178			
White blood cells	0.0706			
Cervix	0.0251			
	0.0106			

FETUS  
% frequency

Development	0.0139
Gastrointestinal	0.0139
Brain	0.0125
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0217
Suprarenal gland	0.0254
Kidney	0.0185
Placenta	0.0303
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0272
Ovary_n	0.0000
Ovary_t	0.0557
Endocrine tissue	0.0245
Fetal	0.0402
Gastrointestinal	0.0610
Hematopoietic	0.0342
Skin-muscle	0.0486
Testicles	0.0309
Lung	0.0328
Nerves	0.0100
Prostate	0.0274
Sensory Organs	0.0310
Uterus_n	0.0291

00673395-122700

## Electronic Northern for SEQ. ID NO.: 44

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0026	0.0019	1.3611	0.7347
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0017	0.0000	undef	0.0000
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0007	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0000	0.0020	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

002221-5667960

Electronic Northern for SEQ. ID NO.: 45

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0013	0.0094	0.1361	7.3472
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0017	0.0100	0.1698	5.8889
Gastrointestinal	0.0134	0.0093	1.4496	0.6898
Brain	0.0052	0.0062	0.8400	1.1905
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0412	0.1285	7.7824
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0052	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0087	0.0085	1.0236	0.9769
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0152	0.0204	0.7482	1.3366
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0040
Placenta	0.0182	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

002227-5627960



Electronic Northern for SEQ. ID NO.: 46

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0107	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

002227 5652960

Electronic Northern for SEQ. ID NO.: 47

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0000	undef	0.0000
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0015	0.0010	1.4399	0.6945
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

002227 5652960

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0015	0.0010	1.4399	0.6945	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0011	0.0000	undef	0.0000	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0010	0.0000	undef	0.0000	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.2111	0.0000	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0030				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 49

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0013	0.0000	undef	0.0000	
Small intestine	0.0000	0.0165	0.0000	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0017	0.0050	0.3396	2.9444	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0010	0.0000	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0030	0.0000	undef	0.0000	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS  
% frequency

Development	
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0036
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0204
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

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Electronic Northern for SEQ. ID NO.: 50

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

00673395 122700

Electronic Northern for SEQ. ID NO.: 51

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.1583	0.0000	undef	
Uterus-endometrium	0.0000	0.0000	undef	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000				
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

00673395.122700

Electronic Northern for SEQ. ID NO.: 52

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0125	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0044	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0006
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0040
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

002227 56554960

Electronic Northern for SEQ. ID NO.: 53

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0051	0.7627	1.3111
Small intestine	0.0051	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0034	0.0025	1.3585	0.7361
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0015	0.0031	0.4800	2.0835
Skin	0.0067	0.0000	undef	0.0000
Hepatic	0.0441	0.0000	undef	0.0000
Heart	0.0048	0.0065	0.7353	1.3600
Testicles	0.0064	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0020	0.5080	1.9684
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0060	0.2856	3.5020
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0267	0.0000	undef
Uterus-endometrium	0.0044	0.0000	undef	0.0000
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0954	0.0000	undef
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0000			

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0254
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0077
Lung	0.0082
Nerves	0.0010
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

00673395-12200



Electronic Northern for SEQ. ID NO.: 54

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0106	0.2047	4.8846
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0000

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder					
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0013	0.0019	0.6805	1.4694	
Ovary	0.0031	0.0000	undef	0.0000	
Endocrine tissue	0.0060	0.0026	2.3025	0.4343	
Gastrointestinal	0.0017	0.0050	0.3396	2.9444	
Brain	0.0057	0.0093	0.6213	1.6096	
Hematopoietic	0.0022	0.0041	0.5400	1.8520	
Skin	0.0027	0.0000	undef	0.0000	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0048	0.0000	undef	0.0000	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0117	0.0000	undef	
Stomach-esophagus	0.0010	0.0020	0.5080	1.9684	
Muscle-skeleton	0.0000	0.0077	0.0000	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0054	0.0068	0.7930	1.2610	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0087	0.0000	undef	0.0000	
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000	0.0000	undef	undef	
Prostate hyperplasia	0.0030				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix	0.0000				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0030
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus n	

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0117	0.0128	0.9153	1.0926
Small intestine	0.0051	0.0132	0.3889	2.5715
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0208	0.0000	undef
Gastrointestinal	0.0102	0.0125	0.8151	1.2268
Brain	0.0134	0.0046	2.8992	0.3449
Hematopoietic	0.0103	0.0113	0.9163	1.0913
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0194	0.0000	undef
Testicles	0.0085	0.0000	undef	0.0000
Lung	0.0173	0.0234	0.7380	1.3551
Stomach-esophagus	0.0145	0.0123	1.1854	0.8436
Muscle-skeleton	0.0097	0.0077	1.2605	0.7933
Kidney	0.0069	0.0000	undef	0.0000
Pancreas	0.0190	0.0000	undef	0.0000
Penis	0.0050	0.0055	0.8974	1.1143
Prostate	0.0090	0.0000	undef	0.0000
Uterus-endometrium	0.0022	0.0085	0.2559	3.9077
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0076	0.0068	1.1223	0.8911
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0030			
Sensory organs	0.0178			
White blood cells	0.0000			
Cervix	0.0052			
	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0051
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0366
Heart-blood vessels	0.0260	Hematopoietic	0.0000
Lung	0.0107	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

00673395.122700

Electronic Northern for SEQ. ID NO.: 57

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0038	0.0075	0.5104	1.9593
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0078	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0077	0.0185	0.4142	2.4145
Brain	0.0096	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0109	0.0085	1.2795	0.7815
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.1908	0.0000	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0000
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

002221-5662950

Electronic Northern for SEQ. ID NO.: 58

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 59

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0026	1.5254	0.6555
Small intestine	0.0281	0.0226	1.2476	0.8015
Ovary	0.0307	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0026	0.0000	undef
Gastrointestinal	0.0085	0.0000	undef	0.0000
Brain	0.0153	0.0324	0.4733	2.1127
Hematopoietic	0.0044	0.0072	0.6171	1.6205
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0257	0.0000	undef	0.0000
Heart	0.0048	0.0065	0.7353	1.3600
Testicles	0.0032	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Lung	0.0000	0.0061	0.0000	undef
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0154	0.0180	0.8567	1.1673
Kidney	0.0217	0.0068	3.1722	0.3152
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0235			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0476
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0151
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0181	Testicles	0.0000
Kidney	0.0254	Lung	0.0082
Placenta	0.0000	Nerves	0.0050
Prostate	0.0303	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0208

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Electronic Northern for SEQ. ID NO.: 60

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0102	1.5254	0.6555
Breast	0.0115	0.0207	0.5568	1.7960
Small intestine	0.0215	0.0165	1.2976	0.7707
Ovary	0.0240	0.0260	0.9210	1.0858
Endocrine tissue	0.0119	0.0176	0.6792	1.4722
Gastrointestinal	0.0172	0.0139	1.2425	0.8048
Brain	0.0170	0.0246	0.6900	1.4494
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0238	0.0194	1.2255	0.8160
Heart	0.0180	0.0275	0.6553	1.5260
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0156	0.0164	0.9526	1.0498
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0103	0.0060	1.7133	0.5837
Kidney	0.0081	0.0411	0.1983	5.0439
Pancreas	0.0116	0.0055	2.0940	0.4775
Penis	0.0150	0.0267	0.5616	1.7807
Prostate	0.0131	0.0043	3.0709	0.3256
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0061			
Cervix	0.0426			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0157	Fetal	0.0245
Hepatic	0.0000	Gastrointestinal	0.0151
Heart-blood vessels	0.0260	Hematopoietic	0.0122
Lung	0.0213	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0194
Kidney	0.0000	Lung	0.0000
Placenta	0.0062	Nerves	0.0246
Prostate	0.0061	Prostate	0.0211
Sensory organs	0.0000	Sensory Organs	0.0274
	0.0126	Uterus_n	0.0000
			0.0125

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Electronic Northern for SEQ. ID NO.: 61

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0128	0.0000	undef
Breast	0.0000	0.0056	0.0000	undef
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0119	0.0075	1.5849	0.6309
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0059	0.0072	0.8228	1.2153
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0031	0.0020	1.5241	0.6561
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0120	0.1428	7.0040
Kidney	0.0136	0.0000	undef	0.0000
Pancreas	0.0033	0.0276	0.1197	8.3571
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0153	0.0170	0.8957	1.1165
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0106			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0136
Brain	0.0083	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0058
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0036	Skin-muscle	0.0057
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0154
Placenta	0.0124	Nerves	0.0000
Prostate	0.0061	Prostate	0.0030
Sensory organs	0.0249	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 62

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

0073395-122700

## Electronic Northern for SEQ. ID NO.: 63

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0051	1.5254	0.6555
Small intestine	0.0038	0.0094	0.4083	2.4491
Ovary	0.0031	0.0331	0.0927	10.7893
Endocrine tissue	0.0150	0.0208	0.7195	1.3898
Gastrointestinal	0.0136	0.0100	1.3585	0.7361
Brain	0.0230	0.0046	4.9700	0.2012
Hematopoietic	0.0096	0.0082	1.1699	0.8547
Skin	0.0094	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0053	0.0000	undef	0.0000
Lung	0.0173	0.0000	undef	0.0000
Stomach-esophagus	0.0052	0.0041	1.2701	0.7873
Muscle-skeleton	0.0387	0.0077	5.0421	0.1983
Kidney	0.0051	0.0120	0.4283	2.3347
Pancreas	0.0081	0.0274	0.2974	3.3626
Penis	0.0083	0.0110	0.7479	1.3371
Prostate	0.0150	0.0267	0.5616	1.7807
Uterus-endometrium	0.0044	0.0043	1.0236	0.9769
Uterus-myometrium	0.0068	0.2111	0.0320	31.2422
Uterus-general	0.0076	0.0068	1.1223	0.8911
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0256			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0235			
Cervix	0.0061			
	0.0000			

FETUS  
% frequency

Development	0.0278
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0236
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0289
Suprarenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0628

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0204
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0228
Skin-muscle	0.0097
Testicles	0.0231
Lung	0.0000
Nerves	0.0100
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0083

00222T"56EEZ960

Electronic Northern for SEQ. ID NO.: 64

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

0067339E-122700

Electronic Northern for SEQ. ID NO.: 65

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0244	0.0137	1.7843	0.5604
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395-122700

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0038	0.0000	undef	
Small intestine	0.0031	0.0000	undef	0.0000	
Ovary	0.0000	0.0052	0.0000	undef	
Endocrine tissue	0.0034	0.0000	undef	0.0000	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0022	0.0010	2.1599	0.4630	
Hematopoietic	0.0013	0.0000	undef	0.0000	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0032	0.0000	undef	0.0000	
Testicles	0.0058	0.0000	undef	0.0000	
Lung	0.0010	0.0020	0.5080	1.9684	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0030	0.0000	undef	0.0000	
Prostate	0.0044	0.0000	undef	0.0000	
Uterus-endometrium	0.0000	0.1055	0.0000	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0009				
White blood cells	0.0000				
Cervix					

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

## Electronic Northern for SEQ. ID NO.: 68

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0038	0.0188	0.2042	4.8982
Small intestine	0.0153	0.0331	0.4634	2.1579
Ovary	0.0120	0.0208	0.5756	1.7372
Endocrine tissue	0.0136	0.0125	1.0868	0.9201
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0052	0.0041	1.2599	0.7937
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0847	0.0000	undef
Hepatic	0.0095	0.0194	0.4902	2.0400
Heart	0.0307	0.0275	1.1179	0.8945
Testicles	0.0000	0.0351	0.0000	undef
Lung	0.0042	0.0286	0.1452	6.8893
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0120	0.4283	2.3347
Kidney	0.0054	0.0137	0.3965	2.5219
Pancreas	0.0116	0.0110	1.0470	0.9551
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0106	0.4095	2.4423
Uterus-endometrium	0.0135	0.1583	0.0854	11.7158
Uterus-myometrium	0.0076	0.0204	0.3741	2.6732
Uterus-general	0.0102	0.1908	0.0534	18.7357
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0130			
Cervix	0.0000			

FETUS  
% frequency

Development	0.0557
Gastrointestinal	0.0194
Brain	0.0000
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0108
Suprarenal gland	0.0254
Kidney	0.0000
Placenta	0.0061
Prostate	0.0748
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0105
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0421
Testicles	0.0077
Lung	0.0082
Nerves	0.0030
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0083

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00/22T 5652960

Electronic Northern for SEQ. ID NO.: 69

	NORMAL % frequency	TUMOR % frequency	Ratios N/T      T/N	
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395-122700



	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0019	0.0000	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 71

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0230	0.0000	undef
Breast	0.0051	0.0056	0.9074	1.1021
Small intestine	0.0215	0.0000	undef	0.0000
Ovary	0.0060	0.0182	0.3289	3.0402
Endocrine tissue	0.0068	0.0000	undef	0.0000
Gastrointestinal	0.0728	0.0185	3.9346	0.2542
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0259	0.1838	5.4400
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0114	0.0061	1.8628	0.5368
Stomach-esophagus	0.0387	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0136
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0083	Ovary_t	0.0608
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395-122700

Electronic Northern for SEQ. ID NO.: 72

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.2111	0.0320	31.2422
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0366
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0309	Lung	0.0000
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

00673395-122700

## Electronic Northern for SEQ. ID NO.: 73

	NORMAL	TUMOR	Ratios		
	% frequency	% frequency	N/T	T/N	
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0013	0.0019	0.6805	1.4694	
Small intestine	0.0000	0.0165	0.0000	undef	
Ovary	0.0000	0.0078	0.0000	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0019	0.0000	undef	0.0000	
Brain	0.0007	0.0021	0.3600	2.7779	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0021	0.0000	undef	0.0000	
Testicles	0.0000	0.0234	0.0000	undef	
Lung	0.0021	0.0061	0.3387	2.9526	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0043	0.0000	undef	
Uterus-endometrium	0.0000	0.1055	0.0000	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0030				
Seminal vesicle	0.0000				
Sensory organs	0.0017				
White blood cells	0.0000				
Cervix					

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0136
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0114
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00227" 56554960

Electronic Northern for SEQ. ID NO.: 74

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0051	1.5254	0.6555
Breast	0.0051	0.0075	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0090	0.0000	undef	0.0000
Endocrine tissue	0.0119	0.0125	0.9509	1.0516
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0059	0.0051	1.1519	0.8681
Hematopoietic	0.0187	0.0379	0.4940	2.0241
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0073	0.0041	1.7781	0.5624
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0043	1.5354	0.6513
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0023
Hepatic	0.2513	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0124	Lung	0.0246
Placenta	0.0061	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0083

002227" 56EE2960

## Electronic Northern for SEQ. ID NO.: 75

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0090	0.0078	1.1513	0.8686
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0019	0.0231	0.0828	12.0723
Brain	0.0089	0.0031	2.8798	0.3472
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0031	0.0061	0.5080	1.9684
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0151
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0130
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0060
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0208

006239E 12700 00/22T 5552960

Electronic Northern for SEQ. ID NO.: 76

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.2111	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development 0.0000  
Gastrointestinal 0.0000  
Brain 0.0000  
Hematopoietic 0.0000  
Skin 0.0000  
Hepatic 0.0000  
Heart-blood vessels 0.0000  
Lung 0.0000  
Suprarenal gland 0.0000  
Kidney 0.0000  
Placenta 0.0000  
Prostate 0.0000  
Sensory organs 0.0000

Breast 0.0000  
Ovary\_n 0.0000  
Ovary\_t 0.0000  
Endocrine tissue 0.0000  
Fetal 0.0000  
Gastrointestinal 0.0000  
Hematopoietic 0.0000  
Skin-muscle 0.0000  
Testicles 0.0000  
Lung 0.0000  
Nerves 0.0000  
Prostate 0.0000  
Sensory Organs 0.0000  
Uterus\_n 0.0000

00673395-122700

Electronic Northern for SEQ. ID NO.: 77

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673305 "122700



Electronic Northern for SEQ. ID NO.: 78

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0213			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395-122700

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0013	0.0000	undef	0.0000	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0030	0.0000	undef	0.0000	
Endocrine tissue	0.0017	0.0050	0.3396	2.9444	
Gastrointestinal	0.0019	0.0000	undef	0.0000	
Brain	0.0007	0.0031	0.2400	4.1669	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0048	0.0129	0.3676	2.7200	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0020	0.0000	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0034	0.0000	undef	0.0000	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0055	0.0000	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0044	0.0021	2.0473	0.4885	
Uterus-endometrium	0.0000	0.1583	0.0000	undef	
Uterus-myometrium	0.0000	0.0068	0.0000	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0032				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0118				
White blood cells	0.0000				
Cervix	0.0000				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development	0.0278	Breast	0.0068
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0164
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder					
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0013	0.0000	undef	0.0000	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0055	0.0000	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.1583	0.0000	undef	
Uterus-myometrium	0.0000	0.0068	0.0000	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0032				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix	0.0000				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development	0.0278	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 81

	NORMAL	TUMOR	Ratios		
	% frequency	% frequency	N/T		T/N
Bladder					
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.1055	0.0000	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395-12200

Electronic Northern for SEQ. ID NO.: 82

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0077	0.0150	0.5104	1.9593
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0090	0.0208	0.4317	2.3163
Endocrine tissue	0.0068	0.0150	0.4528	2.2083
Gastrointestinal	0.0268	0.0231	1.1597	0.8623
Brain	0.0081	0.0123	0.6600	1.5152
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0011	0.0412	0.0257	38.9118
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0031	0.0123	0.2540	3.9367
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0103	0.0060	1.7133	0.5837
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0050	0.0166	0.2991	3.3428
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0305	0.0554	0.5512	1.8143
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0000			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development		Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0253
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0507	Lung	0.0082
Placenta	0.0000	Nerves	0.0131
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

00673395-122700

Electronic Northern for SEQ. ID NO.: 83

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395-122700

Electronic Northern for SEQ. ID NO.: 84

	NORMAL	TUMOR	Ratios		
	% frequency	% frequency	N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0019	0.0000	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0022	0.0000	undef	0.0000	
Prostate	0.0000	0.1055	0.0000	undef	
Uterus-endometrium	0.0000	0.0000	undef	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000				
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

004221" 5652960

Electronic Northern for SEQ. ID NO.: 85				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	



## Electronic Northern for SEQ. ID NO.: 86

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

004227 5652960

Electronic Northern for SEQ. ID NO.: 87

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0204	0.1907	5.2444
Breast	0.0128	0.0075	1.7013	0.5878
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0030	0.0078	0.3838	2.6058
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0038	0.0139	0.2761	3.6217
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0149	0.2925	3.4192
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 88

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0050	0.0000	undef
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0007	0.0010	0.7200	1.3890
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0011	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0020	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0017			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 89

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder					
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0013	0.0000	undef	0.0000	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0055	0.0000	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.1583	0.0000	undef	
Uterus-myometrium	0.0000	0.0068	0.0000	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0032				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

00/22T" 55E2960

Electronic Northern for SEQ. ID NO.: 90

	NORMAL % frequency	TUMOR % frequency	Ratios N/T      T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0006
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 91

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0090	0.0038	2.3818	0.4198
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0037	0.0021	1.7999	0.5556
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0847	0.1300	7.6946
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0026			
White blood cells	0.0106			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0050
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

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Electronic Northern for SEQ. ID NO.: 92

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395-122700

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	



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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.2513	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0121	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0208

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000	Breast 0.0000
Gastrointestinal	0.0000	Ovary_n 0.0000
Brain	0.0000	Ovary_t 0.0000
Hematopoietic	0.0000	Endocrine tissue 0.0000
Skin	0.0000	Fetal 0.0000
Hepatic	0.0000	Gastrointestinal 0.0000
Heart-blood vessels	0.0000	Hematopoietic 0.0000
Lung	0.0000	Skin-muscle 0.0000
Suprarenal gland	0.0000	Testicles 0.0000
Kidney	0.0000	Lung 0.0000
Placenta	0.0000	Nerves 0.0000
Prostate	0.0000	Prostate 0.0000
Sensory organs	0.0000	Sensory Organs 0.0000
		Uterus n

## Electronic Northern for SEQ. ID NO.: 96

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000		
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 97

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0055	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000		
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

002221 563395 122700

Electronic Northern for SEQ. ID NO.: 98

	NORMAL	TUMOR	Ratios		
	% frequency	% frequency	N/T		T/N
Bladder	0.0000	0.0026	0.0000	undef	
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0030	0.0026	1.1513	0.8686	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0038	0.0000	undef	0.0000	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0040	0.0000	undef	0.0000	
Skin	0.0330	0.0000	undef	0.0000	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0055	0.0000	undef	
Penis	0.0000	0.0533	0.0000	undef	
Prostate	0.0022	0.0021	1.0236	0.9769	
Uterus-endometrium	0.0000	0.1055	0.0000	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0064		undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0017				
White blood cells	0.0000				
Cervix					

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0030
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T      T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 100

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0020	2.5402	0.3937
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 101

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 102

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 103

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0064	0.0000	undef	0.0000
Ovary	0.0000	0.0165	0.0000	undef
Endocrine tissue	0.0000	0.0078	0.0000	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0015	0.0021	0.7200	1.3890
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0032	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0041	0.2540	3.9367
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0249	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 104

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED	
		% frequency	LIBRARIES	
			% frequency	
Development	0.0000	Breast	0.0000	
Gastrointestinal	0.0000	Ovary_n	0.0000	
Brain	0.0000	Ovary_t	0.0000	
Hematopoietic	0.0000	Endocrine tissue	0.0000	
Skin	0.0000	Fetal	0.0000	
Hepatic	0.0000	Gastrointestinal	0.0000	
Heart-blood vessels	0.0000	Hematopoietic	0.0000	
Lung	0.0000	Skin-muscle	0.0000	
Suprarenal gland	0.0000	Testicles	0.0000	
Kidney	0.0000	Lung	0.0000	
Placenta	0.0000	Nerves	0.0000	
Prostate	0.0000	Prostate	0.0000	
Sensory organs	0.0000	Sensory Organs	0.0000	
		Uterus_n	0.0000	

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Electronic Northern for SEQ. ID NO.: 105

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0090	0.0038	2.3818	0.4198
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0052	0.5756	1.7372
Gastrointestinal	0.0034	0.0025	1.3585	0.7361
Brain	0.0096	0.0000	undef	0.0000
Hematopoietic	0.0037	0.0021	1.7999	0.5556
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0110	0.0847	0.1300	7.6946
Heart	0.0095	0.0065	1.4706	0.6800
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0010	0.0020	0.5080	1.9684
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0026			
Cervix	0.0106			

FETUS  
% frequency

Development	0.0139
Gastrointestinal	0.0111
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0108
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0000
Nerves	0.0050
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0125

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Electronic Northern for SEQ. ID NO.: 106

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 107

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 108

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0051	0.0038	1.3611	0.7347
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0037	0.0062	0.6000	1.6668
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0267	0.1123	8.9035
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0030
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0310
		Uterus_n	0.0042

00673395 "122700

Electronic Northern for SEQ. ID NO.: 109

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 110

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 111

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0051	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0021	1.0799	0.9260
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0106			

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0231
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

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Electronic Northern for SEQ. ID NO.: 112

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0017	0.0000	undef	0.0000
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0022	0.0010	2.1599	0.4630
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

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Electronic Northern for SEQ. ID NO.: 113

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0050	1.0189	0.9815
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0037	0.0062	0.6000	1.6668
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0267	0.2246	4.4517
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0017			
Cervix	0.0000			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0030
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0310
		Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 114

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0038	0.0093	0.4142	2.4145
Brain	0.0022	0.0021	1.0799	0.9260
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0095	0.0412	0.2313	4.3235
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0164	0.1905	5.2490
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0069	0.0180	0.3807	2.6265
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0064	0.3412	2.9308
Uterus-endometrium	0.0068	0.2111	0.0320	31.2422
Uterus-myometrium	0.0000	0.0204	0.0000	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0017			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0087
Hepatic	0.0260	Gastrointestinal	0.0244
Heart-blood vessels	0.0107	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0356
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0061	Nerves	0.0010
Prostate	0.0000	Nerves	0.0000
Sensory organs	0.0000	Prostate	0.0000
		Sensory Organs	0.0250
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 115

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 116

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast				
Small intestine	0.0039	0.0077	0.5085	1.9666
Ovary	0.0128	0.0000	undef	0.0000
Endocrine tissue	0.0061	0.0165	0.3707	2.6973
Gastrointestinal	0.0060	0.0000	undef	0.0000
Brain	0.0068	0.0050	1.3585	0.7361
Hematopoietic	0.0038	0.0046	0.8283	1.2072
Skin	0.0037	0.0051	0.7200	1.3890
Hepatic	0.0027	0.0000	undef	0.0000
Heart	0.0147	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0137	0.3084	3.2426
Stomach-esophagus	0.0058	0.0000	undef	0.0000
Muscle-skeleton	0.0042	0.0041	1.0161	0.9842
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0086	0.0000	undef	0.0000
Penis	0.0054	0.0068	0.7930	1.2610
Prostate	0.0033	0.0000	undef	0.0000
Uterus-endometrium	0.0090	0.0000	undef	0.0000
Uterus-myometrium	0.0022	0.0043	0.5118	1.9538
Uterus-general	0.0068	0.1055	0.0640	15.6211
Breast hyperplasia	0.0076	0.0000	undef	0.0000
Prostate hyperplasia	0.0051	0.0000	undef	0.0000
Seminal vesicle	0.0128			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.0118			
	0.0061			
	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0228
Lung	0.0036	Skin-muscle	0.0227
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0060
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0083

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Electronic Northern for SEQ. ID NO.: 117

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0026	1.5254	0.6555
Small intestine	0.0038	0.0094	0.4083	2.4491
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0052	0.5756	1.7372
Gastrointestinal	0.0000	0.0050	0.0000	undef
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0037	0.0000	undef	0.0000
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0021	0.0137	0.1542	6.4853
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0041	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0044	0.0128	0.3412	2.9308
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0030			
Sensory organs	0.0000			
White blood cells	0.0087			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0456
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 118

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0026	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395 "122700

Electronic Northern for SEQ. ID NO.: 119

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0000	undef	0.0000
Small intestine	0.0013	0.0038	0.3403	2.9389
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0052	0.0000	undef
Gastrointestinal	0.0034	0.0050	0.6792	1.4722
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0007	0.0041	0.1800	5.5559
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0011	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0110
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0155
		Uterus_n	0.0000

00673395 122700

Electronic Northern for SEQ. ID NO.: 120

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0077	2.5424	0.3933
Breast	0.0090	0.0075	1.1909	0.8397
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0068	0.0125	0.5434	1.8403
Gastrointestinal	0.0038	0.0093	0.4142	2.4145
Brain	0.0059	0.0031	1.9199	0.5209
Hematopoietic	0.0027	0.0758	0.0353	28.3379
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0041	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0087	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0000		
Prostate hyperplasia	0.0000	0.0000		
Seminal vesicle	0.0118			
Sensory organs	0.0043			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0228
Lung	0.0071	Skin-muscle	0.0000
Suprarenal gland	0.0145	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0060
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395 " 1.22700

Electronic Northern for SEQ. ID NO.: 121

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395-122700

## Electronic Northern for SEQ. ID NO.: 122

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0234	0.0230	1.0170	0.9833
Breast	0.0269	0.0207	1.2992	0.7697
Small intestine	0.0061	0.0662	0.0927	10.7893
Ovary	0.0150	0.0572	0.2616	3.8219
Endocrine tissue	0.0085	0.0100	0.8491	1.1778
Gastrointestinal	0.0134	0.0463	0.2899	3.4492
Brain	0.0015	0.0092	0.1600	6.2504
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0551	0.0000	undef	0.0000
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0073	0.0286	0.2540	3.9367
Stomach-esophagus	0.0966	0.0077	12.6053	0.0793
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0329	0.1600	0.2059	4.8565
Prostate	0.0087	0.0043	2.0473	0.4885
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0532			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0417	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0146
Hepatic	0.0000	Gastrointestinal	0.0366
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0573
Placenta	0.0121	Nerves	0.0040
Prostate	0.0249	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0000

00673395-122700

Electronic Northern for SEQ. ID NO.: 123

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395.122700

Electronic Northern for SEQ. ID NO.: 124

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0037	0.0010	3.5998	0.2778
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0062	Nerves	0.0100
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
	0.0126	Uterus_n	0.0042

00673395-122700

Electronic Northern for SEQ. ID NO.: 125

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0077	2.5424	0.3933
Breast	0.0064	0.0075	0.8507	1.1756
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0153	0.0226	0.6792	1.4722
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0081	0.0092	0.8800	1.1364
Hematopoietic	0.0067	0.0379	0.1764	5.6676
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0102	0.8129	1.2302
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0103	0.0180	0.5711	1.7510
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0329	0.0000	undef	0.0000
Prostate	0.0153	0.0064	2.3885	0.4187
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0305	0.0136	2.2445	0.4455
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0069			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0157	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0121	Nerves	0.0060
Prostate	0.0249	Prostate	0.0342
Sensory organs	0.0000	Sensory Organs	0.0387
		Uterus_n	0.0250

00222T"5652960



Electronic Northern for SEQ. ID NO.: 126

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0021	0.0000	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0032
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395-122700

Electronic Northern for SEQ. ID NO.: 127

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0312	0.0486	0.6423	1.5569
Breast	0.0192	0.0282	0.6805	1.4694
Small intestine	0.0399	0.0000	undef	0.0000
Ovary	0.0210	0.0364	0.5756	1.7372
Endocrine tissue	0.0290	0.0326	0.8882	1.1258
Gastrointestinal	0.0460	0.0231	1.9880	0.5030
Brain	0.0532	0.0575	0.9257	1.0803
Hematopoietic	0.0348	0.0379	0.9175	1.0899
Skin	0.0367	0.0000	undef	0.0000
Hepatic	0.0048	0.0647	0.0735	13.5999
Heart	0.0699	0.0412	1.6961	0.5896
Testicles	0.0288	0.4210	0.0683	14.6349
Lung	0.0343	0.0368	0.9314	1.0737
Stomach-esophagus	0.0773	0.0230	3.3614	0.2975
Muscle-skeleton	0.0497	0.0660	0.7528	1.3283
Kidney	0.0353	0.1575	0.2241	4.4619
Pancreas	0.0165	0.0939	0.1760	5.6828
Penis	0.0299	0.0267	1.1232	0.8903
Prostate	0.0196	0.0298	0.6580	1.5197
Uterus-endometrium	0.0270	0.1583	0.1707	5.8579
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0505			
Seminal vesicle	0.0890			
Sensory organs	0.0353			
White blood cells	0.0399			
Cervix	0.0319			

FETUS  
% frequency

Development	0.0417
Gastrointestinal	0.0333
Brain	0.0313
Hematopoietic	0.0197
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0783
Lung	0.0217
Suprarenal gland	0.0507
Kidney	0.0309
Placenta	0.0727
Prostate	0.0997
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0082
Gastrointestinal	0.0244
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0077
Lung	0.0082
Nerves	0.0141
Prostate	0.0000
Sensory Organs	0.0310
Uterus_n	0.0125

002221"5662960

Electronic Northern for SEQ. ID NO.: 128

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0077	0.5085	1.9666
Small intestine	0.0038	0.0000	undef	0.0000
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0068	0.0025	2.7170	0.3681
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0007	0.0031	0.2400	4.1669
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0173	0.0117	1.4759	0.6775
Stomach-esophagus	0.0021	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0086	0.0000	undef	0.0000
Pancreas	0.0081	0.0000	undef	0.0000
Penis	0.0033	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0022	0.0043	0.5118	1.9538
Uterus-myometrium	0.0135	0.1055	0.1280	7.8106
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0030			
Sensory organs	0.0089			
White blood cells	0.0235			
Cervix	0.0026			
	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0204
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0152
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0036	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0060
Prostate	0.0061	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0042

00227" 5667960

Electronic Northern for SEQ. ID NO.: 129

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0019	0.0000	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0017	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0007	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Suprarenal gland	0.0254
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0077
Lung	0.0000
Nerves	0.0010
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0000

002221"56E2960

Electronic Northern for SEQ. ID NO.: 130

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

004227 5552960

Electronic Northern for SEQ. ID NO.: 131

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0078	0.0128	0.6102	1.6389
Small intestine	0.0115	0.0169	0.6805	1.4694
Ovary	0.0000	0.0165	0.0000	undef
Endocrine tissue	0.0060	0.0260	0.2303	4.3431
Gastrointestinal	0.0153	0.0176	0.8733	1.1451
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0074	0.0092	0.8000	1.2501
Skin	0.0080	0.0758	0.1059	9.4460
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0095	0.0065	1.4706	0.6800
Testicles	0.0201	0.0000	undef	0.0000
Lung	0.0058	0.0234	0.2460	4.0652
Stomach-esophagus	0.0114	0.0164	0.6985	1.4315
Muscle-skeleton	0.0193	0.0077	2.5211	0.3967
Kidney	0.0051	0.0120	0.4283	2.3347
Pancreas	0.0136	0.0137	0.9913	1.0088
Penis	0.0066	0.0110	0.5983	1.6714
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0065	0.0128	0.5118	1.9538
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0076	0.0000	undef	0.0000
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0089			
Sensory organs	0.0089			
White blood cells	0.0118			
Cervix	0.0009			
	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0204
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0260	Hematopoietic	0.0057
Lung	0.0107	Skin-muscle	0.0259
Suprarenal gland	0.0108	Testicles	0.0077
Kidney	0.0000	Lung	0.0082
Placenta	0.0062	Nerves	0.0090
Prostate	0.0424	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0167

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NORMAL	TUMOR	Ratios	
% frequency	% frequency	N/T	T/N

Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0011	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 133

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0141	0.0150	0.9357	1.0687
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0120	0.0104	1.1513	0.8686
Endocrine tissue	0.0102	0.0176	0.5822	1.7176
Gastrointestinal	0.0057	0.0139	0.4142	2.4145
Brain	0.0052	0.0072	0.7200	1.3890
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0058	0.0234	0.2460	4.0652
Lung	0.0104	0.0204	0.5080	1.9684
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0086	0.0240	0.3569	2.8016
Kidney	0.0244	0.0000	undef	0.0000
Pancreas	0.0066	0.0110	0.5983	1.6714
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0153	0.0149	1.0236	0.9769
Uterus-endometrium	0.0270	0.2111	0.1280	7.8106
Uterus-myometrium	0.0305	0.0136	2.2445	0.4455
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0327			
Seminal vesicle	0.0178			
Sensory organs	0.0235			
White blood cells	0.0000			
Cervix	0.0319			

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0305	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.0253
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0093
Hepatic	0.0520	Gastrointestinal	0.0122
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0253	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0309	Lung	0.0246
Placenta	0.0061	Nerves	0.0020
Prostate	0.0000	Nerves	0.0068
Sensory organs	0.0000	Prostate	0.0000
		Sensory Organs	0.0042
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 134

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0273	0.0383	0.7119	1.4047
Small intestine	0.0141	0.0244	0.5758	1.7366
Ovary	0.0245	0.0331	0.7415	1.3487
Endocrine tissue	0.0120	0.0312	0.3838	2.6058
Gastrointestinal	0.0290	0.0201	1.4434	0.6928
Brain	0.0287	0.0278	1.0354	0.9658
Hematopoietic	0.0133	0.0298	0.4469	2.2378
Skin	0.0281	0.0379	0.7411	1.3494
Hepatic	0.0073	0.0847	0.0866	11.5419
Heart	0.0381	0.0259	1.4706	0.6800
Testicles	0.0191	0.1512	0.1262	7.9265
Lung	0.0173	0.0702	0.2460	4.0652
Stomach-esophagus	0.0447	0.0470	0.9498	1.0528
Muscle-skeleton	0.0773	0.0153	5.0421	0.1983
Kidney	0.0668	0.0420	1.5909	0.6286
Pancreas	0.0190	0.0342	0.5551	1.8014
Penis	0.0066	0.0331	0.1994	5.0142
Prostate	0.0150	0.1600	0.0936	10.6842
Uterus-endometrium	0.0196	0.0149	1.3161	0.7598
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0229	0.0204	1.1223	0.8911
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0030			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.1240			
	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0408
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0111	Ovary_t	0.0253
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0118	Fetal	0.0169
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0260	Hematopoietic	0.0000
Lung	0.0107	Skin-muscle	0.0454
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0000
Prostate	0.0364	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
	0.0126	Uterus_n	

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Electronic Northern for SEQ. ID NO.: 135

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0390	0.0383	1.0170	0.9833
Small intestine	0.0102	0.0301	0.3403	2.9389
Ovary	0.0429	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0156	0.1919	5.2117
Gastrointestinal	0.0358	0.0351	1.0189	0.9815
Brain	0.0115	0.0278	0.4142	2.4145
Hematopoietic	0.0148	0.0226	0.6545	1.5279
Skin	0.0227	0.2273	0.1000	10.0016
Hepatic	0.0367	0.1695	0.2166	4.6168
Heart	0.0285	0.0582	0.4902	2.0400
Testicles	0.0445	0.0687	0.6476	1.5441
Lung	0.0173	0.0234	0.7380	1.3551
Stomach-esophagus	0.0291	0.0470	0.6185	1.6169
Muscle-skeleton	0.0580	0.0153	3.7816	0.2644
Kidney	0.0685	0.0840	0.8159	1.2257
Pancreas	0.0244	0.0685	0.3569	2.8022
Penis	0.0116	0.0607	0.1904	5.2530
Prostate	0.0180	0.0000	undef	0.0000
Uterus-endometrium	0.0131	0.0064	2.0473	0.4885
Uterus-myometrium	0.0135	0.6332	0.0213	46.8633
Uterus-general	0.0076	0.0408	0.1870	5.3463
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0128			
Seminal vesicle	0.0149			
Sensory organs	0.0000			
White blood cells	0.0867			
Cervix	0.0639			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0167
Hematopoietic	0.0000
Skin	0.0236
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0182
Prostate	0.0997
Sensory organs	0.0000

Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0077
Lung	0.0000
Nerves	0.0030
Prostate	0.0000
Sensory Organs	0.0464
Uterus_n	0.0000

00222T 56552960

Electronic Northern for SEQ. ID NO.: 136

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0102	0.0038	2.7221	0.3674
Ovary	0.0092	0.0165	0.5561	1.7982
Endocrine tissue	0.0090	0.0078	1.1513	0.8686
Gastrointestinal	0.0000	0.0150	0.0000	undef
Brain	0.0019	0.0093	0.2071	4.8289
Hematopoietic	0.0059	0.0031	1.9199	0.5209
Skin	0.0040	0.0379	0.1059	9.4460
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0048	0.0065	0.7353	1.3600
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0114	0.0041	2.7942	0.3579
Muscle-skeleton	0.0097	0.0153	0.6303	1.5866
Kidney	0.0103	0.0120	0.8567	1.1673
Pancreas	0.0081	0.0000	undef	0.0000
Penis	0.0050	0.0000	undef	0.0000
Prostate	0.0060	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0064	0.0000	undef
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0104			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0142	Skin-muscle	0.0000
Suprarenal gland	0.0108	Testicles	0.0000
Kidney	0.0254	Lung	0.0164
Placenta	0.0000	Nerves	0.0060
Prostate	0.0061	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0126	Uterus_n	0.0125

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Electronic Northern for SEQ. ID NO.: 137

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0017	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395 122700

## Electronic Northern for SEQ. ID NO.: 138

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0051	3.0509	0.3278
Breast	0.0000	0.0038	0.0000	undef
Small intestine	0.0000	0.0331	0.0000	undef
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0051	0.0050	1.0189	0.9815
Gastrointestinal	0.0077	0.0139	0.5522	1.8109
Brain	0.0059	0.0062	0.9599	1.0417
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0085	0.0275	0.3084	3.2426
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0062	0.0143	0.4355	2.2964
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0137	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0033	0.0276	0.1197	8.3571
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0087			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0108
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0242
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0272
Ovary_n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0151
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0356
Testicles	0.0000
Lung	0.0000
Nerves	0.0090
Prostate	0.0068
Sensory Organs	0.0077
Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 139

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0056	0.2268	4.4083
Ovary	0.0061	0.0165	0.3707	2.6973
Endocrine tissue	0.0120	0.0052	2.3025	0.4343
Gastrointestinal	0.0017	0.0025	0.6792	1.4722
Brain	0.0077	0.0046	1.6567	0.6036
Hematopoietic	0.0000	0.0021	0.0000	undef
Skin	0.0067	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0275	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0041	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Nerves	0.0137
Sensory organs	0.0251	Prostate	0.0000
		Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 140

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0051	0.0094	0.5444	1.8368
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0090	0.0000	undef	0.0000
Endocrine tissue	0.0085	0.0100	0.8491	1.1778
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0015	0.0041	0.3600	2.7779
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0042	0.0020	2.0321	0.4921
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0043	1.0236	0.9769
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0026			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0204
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0116
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 141

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0051	0.0000	undef
Small intestine	0.0064	0.0150	0.4253	2.3511
Ovary	0.0000	0.0496	0.0000	undef
Endocrine tissue	0.0060	0.0026	2.3025	0.4343
Gastrointestinal	0.0068	0.0050	1.3585	0.7361
Brain	0.0096	0.0046	2.0708	0.4829
Hematopoietic	0.0052	0.0051	1.0079	0.9921
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0053	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0083	0.0061	1.3548	0.7381
Muscle-skeleton	0.0000	0.0153	0.0000	undef
Kidney	0.0103	0.0000	undef	0.0000
Pancreas	0.0027	0.0068	0.3965	2.5219
Penis	0.0033	0.0055	0.5983	1.6714
Prostate	0.0120	0.0267	0.4493	2.2259
Uterus-endometrium	0.0000	0.0021	0.0000	undef
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0076	0.0000	undef	0.0000
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0087			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0082
Placenta	0.0061	Nerves	0.0040
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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## 2.2. Fisher Test

In order to decide whether a partial sequence *S* of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to *S*. If the null hypothesis can be rejected with high enough certainty, the gene belonging to *S* is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

### Example 3

#### Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence *S* is completed in three steps:

1. Determination of all sequences homologous to *S* from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence *C* from the assembled sequences.

Consensus sequence *C* will generally be longer than initial sequence *S*. Its electronic Northern Blot will accordingly

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In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

**Example 4****Mapping of Nucleic Acid Sequences on the Human Genome**

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server ([http://www.stanford.edu/RH/rhserver\\_form2.html](http://www.stanford.edu/RH/rhserver_form2.html)). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

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the results were evaluated with the above-mentioned software and the software of the Whitehead Institute  
(<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

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## References to the modules:

Pfam: Protein families database of alignments and HMMs  
(pfam@sanger.ac.uk)

PROSITE: The PROSITE database, its status in 1999. Nucleic  
Acids Res. 27: 215-219 (<http://www.expasy.ch/sprot/prosite.html>)

## TABLE I

Col. 1 - Sequence ID No.:  
Col. 2 - Expression in the endometrial tumor:  
Col. 3 - Function  
Col. 4 - Modules  
Col. 5 - Length of the applied sequence in bases  
Col. 6 - Cytogenetic localization  
Col. 7 - Next marker

## [Key to Table I:]

## [Col. 2:]

[Seq. ID Nos. 1-62] erhöht = elevated

## [Col. 3:]

[Seq. ID Nos.: 1, 7-15, 78-126, 136] unbekannt = unknown

[Seq. ID Nos.: 3, 4, 38, 67-72] Homolog zu... = homologous  
to...

[Seq. ID Nos.: 531-555] Verlängerung von Seq. ID No. ... =  
Lengthening of Seq. ID No. ...

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5 TABELLE I

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
1	erhöht	unbekannt		1046	2p24-2p21	D2S174-D2S390
2	erhöht	Mouse mammary tumor virus proviral envelope gene Polymerase protein	2x "CSD"	373		
3	erhöht	Homolog zu Human protein kinase C-binding protein RACK17		1571	1q32.1	D1S477-D1S504
4	erhöht	Homolog zu Human mRNA for KIAA0079		1789	10q21.3-q22.2	D10S537-D10S218
5	erhöht	Caenorhabditis elegans cosmid T23B12	"BTB"	2361		
6	erhöht	Caenorhabditis elegans cosmid C01A2		1638	20q13.32-q13.33	D20S100-D20S173
7	erhöht	unbekannt		1034	12q12	D12S1589-D12S85
8	erhöht	unbekannt		947	17p11.2-p12	AFMa126yd5
9	erhöht	unbekannt		497		
10	erhöht	unbekannt		269		
11	erhöht	unbekannt		1717		
12	erhöht	unbekannt	"zf-C3HC4"	1419		
13	erhöht	unbekannt		671	2q37.3	D2S2704
14	erhöht	unbekannt		524		
15	erhöht	unbekannt		345		
16	erhöht	rGSTK1-1=glutathione S-transferase subunit 13		1060	7q33-7q36.1	WI-9353
17	erhöht	Rattus norvegicus neuritin		1721	6p23-p25.1	D6S1617-D6S1674
18	erhöht	Rattus norvegicus cytosolic NADP-dependent isocitrate dehydrogenase	"isodh"	2367	2q34	WI-1247
19	erhöht	Rat unr mRNA for unr protein with unknown function	2x "CSD"	1321	1p13.3-1q11	D1S418-D1S252
20	erhöht	Rat prostatic binding protein polypeptide c1		384		
21	erhöht	Rat GTP-binding protein (ral B)		367		
22	erhöht	R.norvegicus mRNA for TRAP-complex gamma subunit		2621	3q24-q25.2	D3S1570
23	erhöht	P. sativum mRNA for Cop1 protein	2x "G-beta"	2019	1q23.3-q24.3	D1S242-D1S416
24	erhöht	P. falciptarum pfmdr1 gene		1866	18q12.1-q12.3	AFM164ya9
25	erhöht	ORF 5' of ECLF2... ECRF3=G protein-coupled receptor homolog		1189		

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
26	erhöht	O.cuniculus lambda-crystallin mRNA	"3HCDH"	1418		
27	erhöht	Mus musculus flotillin		814		
28	erhöht	Mouse glycerol-3-phosphate acyltransferase		3039	10q25.1-q25.2	D10S1465
29	erhöht	Mouse clathrin-associated protein (AP47)	"Adap_comp_sub"	1448		
30	erhöht	Lycopersicon esculentum biotin-containing subunit of methylcrotonyl-CoA carboxylase	"CPSase_L_chain", "biotin_req_enzy"	1394		
31	erhöht	Leucine aminopeptidase, bovine	"Peptidase_M17"	734		
32	erhöht	Klebsiella pneumoniae possible RNA helicase (dead)	2x "DEAD"	692		
33	erhöht	Human mammaglobin Homolog	"Uteroglobulin"	517		
34	erhöht	Human DNA sequence from PAC 138A5 on chromosome X		322		
35	erhöht	Human DNA sequence from clone 230G1		1559		
36	erhöht	Human DNA sequence from clone 217C2		1072		
37	erhöht	Human Cosmid Clone 26a1	"RhoGAP"	454	22.q11.21-q11.23 3p21.1	D22S420-D22S446
38	erhöht	Homolog zu Human chromosome 3p21.1 gene sequence		700		
39	erhöht	Homo sapiens DNA from chromosome 19-cosmid f21246		914		
40	erhöht	H.sapiens mRNA for Plg-1 protein		1669	17q21.31-q21.33	D17S791-D17S797
41	erhöht	H.sapiens CpG island DNA genomic Mse1 fragment		355		
42	erhöht	H.sapiens (TL5) mRNA from LNCaP cell line		2628	3q24	D3S3413
43	erhöht	Genomic sequence from Human 9q34		2535	9q34.11-q34.13	D9S179-D9S164
44	erhöht	Drosophila melanogaster misato gene	"MYB_3"	805	1q21.2	D1S305-D1S506
45	erhöht	Chicken mRNA for vitellogenin I		1279		
46	erhöht	Caenorhabditis elegans DNA from clone F31D4		1923		
47	erhöht	Caenorhabditis elegans cosmid ZK863		706		
48	erhöht	Caenorhabditis elegans cosmid ZK863		749		
49	erhöht	Caenorhabditis elegans cosmid ZK596		857	10q26.13	D10S212
50	erhöht	Caenorhabditis elegans cosmid T26A5		268		
51	erhöht	Caenorhabditis elegans cosmid T21G5		297		
52	erhöht	Caenorhabditis elegans cosmid F56D5		590		
53	erhöht	Caenorhabditis elegans cosmid F25D7		1714		
54	erhöht	Caenorhabditis elegans cosmid F08C6		1340		
55	erhöht	C.botulinum bont (partial) and ninth genes		765	3q24-q23	D3S3409

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogetische Lokalisation	nächster Marker
56	erhöht	Bovine mRNA fragment for 49 kDa subunit of mitochondrial NADH:ubiquinone oxidoreductase (EC 1.6.5.3)	"complex1_4 9Kd"	1647		
57	erhöht	Bos taurus (clone pTKD7) dopamine and cyclic AMP-regulated neuronal phosphoprotein (DARPP-32)		1166		
58	erhöht	A. thaliana mRNA for RNA helicase		487		
59	erhöht	A. thaliana glycine-rich protein (clone atGRP-4)		1630	5q23.3-q31.1	D5S396-D5S2119
60	erhöht	Saccharomyces cerevisiae Grd19p (GRD19)	2x "PX"; "BEM_DOM AIN"	1272	6q21	AFMa191wd1
61	erhöht	Saccharomyces cerevisiae chromosome XII cosmid 9328	2x "DEAD"; "helicase_C"	1914	7p12.3-p13	D7S667-D7S2427
62	erhöht	S. pombe chromosome I cosmid c13D6		608		
63		Rattus norvegicus RNA helicase with arginine-serine-rich domain		2674	17q21.31-q22	D17S797-D17S788
64		Rattus norvegicus matrixin (MMP-7) mRNA		326		
65		Rattus norvegicus Diphor-1	2x "PDZ"	888	1q12	D1S2669-D1S498
66		Human herpesvirus-7 (HHV7) J1, G protein-coupled receptor (GCR)		202		
67		Homolog zu Human synapsin I (SYN1)		1225	1p22.3-p31.1	WI-3099
68		Homolog zu Human PAX3 gene		1093		
69		Homolog zu Human multiple exostosis 2 (EXT2)		309	1p21.3-p22.1	D1S2166
70		Homolog zu Homo sapiens integrin variant beta4E (ITGB4)		380		
71		Homolog zu Homo sapiens hCPE-R mRNA for CPE-receptor		1253		
72		Homolog zu H. sapiens mRNA for deoxyguanosine kinase		439		
73		Caenorhabditis elegans cosmid Y48E1B		1252	4p11-q12	D4S1619-D4S1600
74		Caenorhabditis elegans cosmid T21D12	"WW_DO-MAIN 2"	695		
75		Caenorhabditis elegans cosmid R107		2514	13q33.3-q34	D13S261-D13S293
76		Caenorhabditis elegans cosmid M04C9		274		
77		Bovine opsin	"7Im_1"	449		
78		unbekannt		346		
79		unbekannt		1329		
80		unbekannt		805		



Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cylogenetische Lokalisation	nächster Marker
81		unbekannt		420		
82		unbekannt		2143	9q21.32-q22.1	D9S264-D9S257
83		unbekannt		450		
84		unbekannt		408	17q23.1-q23.2	D17S1680
85		unbekannt		311		
86		unbekannt		487		
87		unbekannt		1902	11p12-p13	WI-6150
88		unbekannt		1048	1q42.11-q43	WI-9317
89		unbekannt		804		
90		unbekannt		581		
91		unbekannt		2042		
92		unbekannt		430		
93		unbekannt		592		
94		unbekannt		674		
95		unbekannt		324		
96		unbekannt		709	5p15.33	D5S1954
97		unbekannt		562		
98		unbekannt		1948	16p13.2-p12.3	D16S499
99		unbekannt		483		
100		unbekannt		437		
101		unbekannt		359		
102		unbekannt		501		
103		unbekannt		1102	1q23.1-q23.2	D1S445-D1S431
104		unbekannt		306		
105		unbekannt		2042		
106		unbekannt		320		
107		unbekannt		506		
108		unbekannt		1276		
109		unbekannt		373		
110		unbekannt	TPR_RE-PEAT™	492		
111		unbekannt		1678	6q21	D6S278-D6S302
112		unbekannt		866	9q22.1-q22.2	D9S1841-D9S196
113		unbekannt		1434	18q12.1-q12.3	D18S1124-D18S468
114		unbekannt		914	7q32.3	D7S686-D7S530
115		unbekannt		685	8p12-p11.23	D8S1821-D8S255

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
116		unbekannt		2646		
117		unbekannt		2667		
118		unbekannt		544		
119		unbekannt		1340	18p11.21	D18S471-D18S464
120		unbekannt		2376		
121		unbekannt		225		
122		unbekannt		1967	6q22.33-q23.1	D6S292-D6S1699
123		unbekannt		612		
124		unbekannt		1183	2q32.3-q34	D2S315-D2S2237
125		unbekannt		891	4q28.1-q31.1	
126		unbekannt		482		
127		Human triosephosphate isomerase mRNA		610		
128		Human ras inhibitor mRNA		2072	9q33.3-q34.11	
129		Human R kappa B		980		
130		Human putative interferon-related protein (SM15)		792		
131		Human protein trafficking protein (S31iii125)	2x "EMP24_GP25L"	1092	14q32.2-14q32.33	WI-9179
132		Human protein kinase C-binding protein RACK7		1523	20q13.13-q13.2	D20S957
133		Human gene for histone H1(0)	"linker_histone"	2241	22q13.1	
134		Human cathepsin B proteinase	"Cys-protease"	631		
135		Homo sapiens cathepsin B mRNA	"Cys-protease"	980		
136		unbekannt		2238	14q24.1-14q24.3	D14S277
137		H.sapiens XG mRNA		398		
138		H.sapiens mRNA for RAB7 protein	ras	1084	7q21.3-q22.1	D7S652
139		H.sapiens mRNA for pyrroline 5-carboxylate synthetase		1259		
140		H.sapiens mRNA for beta-1,4-galactosyltransferase		1938	1q22-q23.1	
141		H.sapiens IL-13Ra		1874	Xq23	
531		Verlängerung von Seq. ID No. 19	2x "CSD"	1708	1p13.3-1q11	D1S418-D1S252
532		Verlängerung von Seq. ID No. 23	2x "G-beta"	2128	1q23.3-q24.3	D1S242-D1S416
533		Verlängerung von Seq. ID No. 25		2640		
534		Verlängerung von Seq. ID No. 32	2x "DEAD"	1245		
535		Verlängerung von Seq. ID No. 34		822		

Sequenz ID No.:	Expression im Endometrium- Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
536		Verlängerung von Seq. ID No. 43		2703	9q34.11-q34.13	D9S179-D9S164
537		Verlängerung von Seq. ID No. 44	"MYB_3"	2664	1q21.2	D1S305-D1S506
538		Verlängerung von Seq. ID No. 52		3888		
539		Verlängerung von Seq. ID No. 54		3304		
540		Verlängerung von Seq. ID No. 55		863	3q24-q23	D3S3409
541		Verlängerung von Seq. ID No. 59		1962	5q23.3-q31.1	D5S396-D5S2119
542		Verlängerung von Seq. ID No. 60	2x "PX"; "BEM_DOM AIN"	1772	6q21	AFMa191wd1
543		Verlängerung von Seq. ID No. 65	2x "PDZ"	1009	1q12	D1S2669-D1S498
544		Verlängerung von Seq. ID No. 69		2834	1p21.3-p22.1	D1S2166
545		Verlängerung von Seq. ID No. 82		2319	9q21.32-q22.1	D9S264-D9S257
546		Verlängerung von Seq. ID No. 84		2456	17q23.1-q23.2	D17S1680
547		Verlängerung von Seq. ID No. 87		2218	11p12-p13	WI-6150
548		Verlängerung von Seq. ID No. 88		2196	1q42.11-q43	WI-9317
549		Verlängerung von Seq. ID No. 93		701		
550		Verlängerung von Seq. ID No. 98		2214	16p13.2-p12.3	D16S499
551		Verlängerung von Seq. ID No. 108		1434		
552		Verlängerung von Seq. ID No. 111		2434	6q21	D6S278-D6S302
554		Verlängerung von Seq. ID No. 114		1457	7q32.3	D7S686-D7S530
555		Verlängerung von Seq. ID No. 126		741		

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
1	142
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2	145
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4	151
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8	163
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11	172
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12	175

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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24	211

00/00/00" 5666/960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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25	214
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27	220
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004221" 56552960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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36	248
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37	250
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39	256
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0042227" 56EE2960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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56	308
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00/22T" 56EE2960



DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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71	354

00/222T"56EEZ960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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93	423
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002221" 56EE/960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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103	454
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104	457
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105	461

002221" 56552960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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106	464
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107	466
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108	470
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002221" 56EE2960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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125	523
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126	526
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531	561
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532	564
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004221 56E2960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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533	567
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534	570
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542	594
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543	597
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544	600
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DDC21 566/960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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546	606
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552	624
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554	630
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00422T" 56E2960



The inventive nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 142-528 are described in the following sequence protocol.

### Sequence Protocol

#### (1) GENERAL INFORMATION:

##### (i) APPLICANT:

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Uterus Tumor Tissue

(iii) Number of sequences: 622

##### (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

004227" 56E2960

## (2) INFORMATION ON SEQ ID NO. 1:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1046 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

tcggaacgag ggatcactaa tcaacaaaacc agcttttcggg gtctgacgcg atccttgccct 60
caggcctctc gaggtccaga cagccgcccc gcccgcctctg cgacgcagca gtgaatagtg 120
tggtacctcc ttgtctcggg tcaggtccag acctccccgt cttccggctg ccctgaacgt 180
caggcgacct caggaccctg tgattggcgc ctgcgcgggc ggaccgtgac cgaggaaacc 240
cctggaggga cttgggcatt ccttgggctc cgtgcctgtt cttcgtgctc ctttcggggc 300
aaggatctca cattatcagt ctttgaccga cacagaatgc ctggcatttg ataaatgttt 360
gttgaacttg aagagacata tggacaatga atctgcaaag atactgggga gagataccaa 420
tatcatcaag ccagaccaac agaagttcct tcgatttgct cccacgggag ttccgtcttg 480
tggaagtcca tgacccaccc ctgcaccaac cctcagccaa caagccgaag cccccacta 540
tgctggacat cccctcagag ccatgtagtc tcaccatcca tacgattcag ttgattcagc 600
acaaccgacg tcttcgcaac cttattgcca cagctcaggc ccagaatcag cagcagacag 660
aaggtgtaaa aactgaagag agtgaacctc ttccctcgtg ccctgggtca cctcctctcc 720
ctgatgacct cctgccttta gattgtaaga atcccaatgc accattccag atccggcaca 780
gtgaccacga gagtgacttt tatcgtggga aaggggaaacc tgtgactgaa ctccagctggc 840
actcctgtcg gcagctcctc taccaaggca gtggcacaaa tcttggccaa cggcgggctt 900
ttgactgtgc taatgagagt gtcctggaag accctaactt gatgttggca catgagtatt 960
ggccttaaaag tttaccaaag tttgctgcgt ttttgctgtt gagcggaag cccgggtggg 1020
agagacttcc ttttgccgaa tgtgat
1046

```

## (2) INFORMATION ON SEQ ID NO. 2:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 373 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

004227 9637960

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

cgaaggcaga gttcaacagg gatcttttgt aaatgttcaa caagggccac aggagccatt 60  
tattgaattt atccatcagt taaccaggc aattaagagc acacatggaa catcgaccat120  
tccacgggta tctcgtataa cctcgaagga caagccatag tggaacgttg cccattccac180  
gcttaaaaaat atgcttttaa aaaaggggga atatgaataa ggaccctaca acactactag240  
cacaagtgtt attcaccctt aatttcttaa atttagataa ttaaatttcc aatcagccct300  
agaaaagcac ttttgcttaa aacctcccca ggtagcaagg ctttcagtgt tttgggaagg360  
tgtaatatgt atc 373

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1571 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

09673395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

ctgctctggc aaccaataga agctaggaga gggcggggac aactgggtct tttgcggctg 60
cagcgggctt gtaggtgtcc ggctttgctg gccagcaag cctgataagc atgaagctct 120
tatctttggt ggctgtggtc ggggtgttgc tgggtgcccc agctgaagcc aacaagagtt 180
ctgaagatat ccggtgcaaa tgcattctgtc caccttatag aaacatcagt gggcacattt 240
acaaccagaa tgtatcccag aaggactgca actgcctgca cgtgggtggag cccatgccag 300
tgccctggcca tgacgtggag gcctactgcc tgctgtgcga gtgcaggtag gaggagcgca 360
gaccaccacc atcaaggtca tcattgtcat ctacctgtcc gtgggtgggtg ccctgttgct 420
ctacatggcc ttccctgatgc tgggtggacc tctgatccga aagccggatg catacactga 480
gcaactgcac aatgaggagg agaattgagga tgctcgtctt atggcagcag ctgctgcatt 540
cctcggggga ccccgagcaa acacagtcct ggagcgtgtg gaagggtgcc agcagcgggtg 600
gaagctgcag gtgcaggagc agcgggaagac agtcttcgat cggcacaaga tgctcagcta 660
gatgggctgg tgtggttggg tcaaggcccc aacaccatgg ctgccagctt ccaggctgga 720
caaagcaggg ggctacttct ccttccctc gggtccagtc ttccctttaa aagcctgtgg 780
catttttctt ccttctccct aacttttaga atgttgtact tggctatttt gattagggaa 840
gagggatgtg gtctctgac tccgttgtct tcttgggtct ttggggttga agggaggggg 900
aaggcaggcc agaagggaat ggagacattc gaggcggcct caggagtgga tgcgatctgt 960
ctctcctggc tccactcttg ccgccttcca gctctgagtc ttgggaatgt tgttaccctt 1020
ggaagataaa gctgggtctt caggaactca gtgtctggga ggaaagcatg gccagcatt 1080
cagcatgtgt tcctttctgc agtggttctt tatcaccacc tccctcccag cccagcgcc 1140
tcagccccag cccagctcc agccctgagg acagctctga tgggagagct gggccccctg 1200
agcccaactg gtcttcaggg tgcactggaa gctgggtgtc gctgtccct gtgcacttct 1260
cgcaactggg catggagtgc ccatgcatac tctgctgccg gtccctcac ctgcacttga 1320
ggggtctggg cagtccttcc tctccccagt gtccacagtc actgagccag acggtcgggt 1380
ggaacatgag actcgaggct gagcgtggat ctgaacacca cagccctgt acttgggttg 1440
cctctgttcc ctgaacttcg ttgtaccagt gcatggagag aaaattttgt cctctgttct 1500
tagagtgtg tgtaaatcaa ggaagccatc attaaattgt tttattttct tccaaaaaaa 1560
aaaaaaaaa a 1571

```

## (2) INFORMATION ON SEQ ID NO. 4:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1789 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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agaccatgct ggaaaaaatt ccaaaggaag agcaagaaga gacgtctgca attcgagtgg 60
gttttatcac atataacaaa gttctccatt tctttaatgt gaagagtaat ctggcccagc 120
ctcagatgat gggggtgact gatgttgagg aagtctttgt tcctttgttg gatggtttcc 180
ttgtcaacta tcaagaatcc caatctgtga ttcataattt gttggaccag attccagaca 240
tgtttgacaga ctctaataa aatgagactg tctttgctcc tgtcatccag gctggcatgg 300
aagcactaaa ggcagcagac tgtcctggga agctgttcat cttccattct tccttgccaa 360
ctgctgaagc accaggaag ctcaaaaaa gagatgacaa aaaactggtt aatacagaca 420
aagagaagat acttttccag ccccaaacia atgtctatga ctcatggcc aaggactgag 480
tggtctaccg gctgctctgt gacactcttc ctctttccta gtcagtatgt ggacgtggcc 540
tcgctggggc tggttcctca gctcactgga ggaacccttt acaaatacaa caatttccag 600
atgcacttgg atagacaaca atttttgaac gacctcagaa atgatattga aaagaaaata 660
ggctttgatg ctattatgag ggttcgtacc agcacagggt tcagagccac tgatttcttt 720
ggtggaatct tgatgaacaa caccaccgat gtagaaatgg ctgccatcga ttgtgacaag 780
gcagtgaccg tggagttcaa gcacgatgac aaactcagtg aagacagtgg agccttaatc 840
cagtggtgtg tgctttacac gacaatcagt ggtcaaagaa gacttcggat tcacaatctt 900
ggcttaaaact gcagctctca gctagctgat ctttataaga gctgtgagac agatgctctt 960
atcaacttct ttgccaaagt agctttttaa gcagttctcc accagccttt gaaggtcatc 1020
cgggaaattc tagttaatca gactgcccac atgttggtcat gttaccggaa gaattgtgca 1080
agtcttcttg cagcaagcca gcttattcta ccagattcca tgaaagtatt gccagtgtac 1140
atgaattgct tgttgaaaaa ctgtgtacta ctcagcagac cagagatctc aactgatga 1200
cgagcatacc agagacagct ggtcatgacc atgggtgttg ctgactctca gcttttcttc 1260
taccacaac ttctgcccac acacacgtta gatgtcaaga gtacaatgtt acctgctgcc 1320
gttcgttgct ctgagtcccg tctttcagaa gaaggaatat tcttactggc taatggtcta 1380
cacatgttcc tgtggttggg agtaagcagc ccaccagaac tgatccaagg aatattta 1440
gtgccatctt ttgcacatat caacacagat atgacattgc tgctgaagt gggaaaccca 1500
tactctcaac aactcagaat gataatgggt attatccaac aaaagaggcc atattcaatg 1560
aagctcacia ttgtaaagca gcgagaacaa ccagaaatgg ttttccgaca gttcctggta 1620
gaagacaaaag gactttacgg aggtcttctt tatgtggatt tcctttgttg tgttcacaag 1680
gagatctgtc agctgcttaa ttaattggaa actccccggg caatggaggt tgcgttgcca 1740
gggggggaaa agcccccttt tggggcccaa atttgccagg gggaaaaag 1789

```

## (2) INFORMATION ON SEQ ID NO. 5:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2361 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

0967395.12700

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

gggccagccg	gctcgcccg	gggccatggc	agcagcggt	actgcagccg	agggggtccc	60
cagtcggggg	cctcccgggg	aagtcattcca	tctgaattgtg	ggagccaaga	gattcagtag	120
ctctcgccag	actctcacc	ggatcccaga	ctccttcttc	tccagctctc	tgagcgagacg	180
catctcgacg	ctgaaagatg	agaccggagc	aatcttcatc	gacagggacc	ctacagctctt	240
cgcccccatc	ctcaacttcc	tgcgcaccaa	agagttggat	cccaggggtg	tccacggttc	300
cagcctcctc	catgaagccc	agttctatgg	gtcactcct	ctggttcgtc	gcctgcagct	360
tcgagaggag	ttggatcgat	cttcttgtgg	aaacgtcctc	ttcaatgggt	acctgccgcc	420
accagtgttc	ccagtgaaagc	ggcggaaaccg	gcacagccta	gtggggcctc	agcagctagg	480
aggacggcca	gccccgtctc	gacggagcaa	cacgatgcc	cccaaccttg	gcaatgcagg	540
gctgctgggc	cgaatgctgg	atgagaaaac	ccctccctca	ccctcaggac	aacctgagga	600
gccgggggatg	gtgcgcctgg	tgtgtggaca	ccataattgg	atcgctgtgt	cctataccca	660
gtttctagtc	tgctacaggt	tgaaggaagc	ctctggcggg	cagctgggtg	tttccagccc	720
ccgcctggac	tggcccatgc	gaacgactgg	cgcttcacag	cccggtgca	tgtggggct	780
ttgggtgaac	atgacaagat	ggtggcagca	gccaccggca	gcgagatcct	gctatgggct	840
ctgcaggcgg	aaggcggtgg	ctccgagata	ggggtctttc	atctgggggt	gcctgtggag	900
gccttgtttc	tcgctcgggaa	ccagctcatt	gctacaagcc	acacagggcg	catcggggtg	960
tggaaatgcc	tcaccaagca	ctggcaggtc	caggaggtgc	agcccatcac	cagttatgac	1020
gcggcaggct	cctctcctc	cttgggtgc	aacaacggct	ccatttacta	cgtggatgtg	1080
cagaagttcc	ccttgccgat	gaaagacaac	gacctctgtg	tcagcgagct	ctatcgggac	1140
ccagcggagg	atggggtcac	cgccctcagt	gtctacctca	ccccaaagac	cagtgacagt	1200
gggaactgga	tcgagatcgc	ctatggcacc	agctcagggg	gcgtgcgggt	catcgtgcag	1260
caccocggaga	ctgtgggctc	ggggcctcag	ctcttccaga	ccttcactgt	gcaccgcagc	1320
cctgtcacca	agatcatgct	gtcggagaag	cacctcatct	cagtcctgtgc	cgacaacaac	1380
cacgtgcgga	catggtctgt	gactcgcttc	cgcgccatga	tttccaccca	gcccggtcc	1440
accccaactcg	cttcccttaa	gatcctggct	ctggagtcgg	cagatgggca	tggcggtgc	1500
agtgcctggca	atgacattgg	cccctacggt	gagcgggacg	accagcaagt	gttcatccag	1560
aagggtggtgc	ccagtgccag	ccagctcttc	gtgcgtctct	catctactgg	gcagcgggtg	1620
tgctccgtgc	gctccgtgga	cggctcacc	acgacagcct	tcacagtgtc	ggagtgcgag	1680
ggctcccggc	ggctcggctc	tggccccggg	cgctacctgc	tcactggcca	ggccaacggc	1740
agcttggcca	tgtgggacct	aaccaccgcc	atggacggcc	tggccaggc	ccctgcaggt	1800
ggcctgacgg	agcaagagct	gatggaacag	ctggaacact	gtgagctggc	cccgccggct	1860
ccttcagctc	cctcatgggg	ctgtctcccc	agccctcac	ccgcctctc	cctcaccagc	1920
ctccactcag	cctccagcaa	cacctccttg	tctggccacc	gtgggagccc	aagccccccg	1980
caggctgagg	ccgggcgcgg	tggtgggggg	agctttgtgg	aacgctgcca	ggaactggtg	2040
cggagtgggc	cagacctccg	acggcccaac	acaccagccc	cgtggccctc	cagcgggtctc	2100
ggcactcccc	tcacacctcc	caagatgaa	ctcaatgaaa	cttccctttg	aacaacgcag	2160
ctgccatgat	gccttgggat	ccactggctc	tgggggacct	aggtgcctcc	ctgattcctg	2220
tgggaacccc	gggttcaggg	ccagggcctc	cttggaaata	atggttattg	ttactaggtc	2280
cccaccttcc	ctctttttctg	gaagccaaa	tcacctcccc	caataaagtc	ctcactgcca	2340
aaaaaaaaaa	aaaaaaaaacc	g				

## (2) INFORMATION ON SEQ ID NO. 6:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1638 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

ggctgcggtat ttcgcccgaag atcccgcgaag tgacagcttt ggggggtttgc tgctggctct 60
gactcccgtc ctgcatggtg ttgacgacgg ggaacaatcc ccaagaggca tgaactggtg 120
aagggggccga agaaggttga gaagggtcga aaagatgctg aattagtggc ccaatggaac 180
tattgtactc taagtcagga aatattaaga cgaccaatag ttgcctgtga acttggcaga 240
ctttataaca aagatgccgt cattgaattt ctcttggaac aatctgcaga aaaggctctt 300
gggaaggcag catctcacat taaaagcatt aagaatgtga cagagctgaa gctttctgat 360
aatcctgcct gggaagggga taaaggaaac actaaagggtg acaagcacga tgacctccag 420
cggggcgctt tcatctgccc cggtgtgggc ctggagatga acggccgaca cagggttctgc 480
ttccttcggt gctgcggtg tgtgttttct gagcgagcct tgaaaagatg aaaagcggaa 540
gtttgccaca cgtgtggggc tgccttccag gaggatgatg tcatcgtgct caatggcacc 600
aaggaggatg tggacgtgct gaagacaagg atggaggaga gaaggctgag agcgaattgg 660
aaaagaaaac aaagaaaccc aaggcagcag agtctgtttc aaaaccagat gtcagtgaag 720
aagccccagg gccatcaaaa gttaagacag ggaagcctga agaagccagc cttgattcta 780
gagagaagaa aaccaacttg gctcccaaaa gcacagcaat gaatgagagc tcttctggaa 840
aagctgggaa gcctccgtgt ggagccacaa agaggtccat cgctgacagt gaagaatcgg 900
aggcctacaa gtccctcttt accactcaca gctccgcca gctcctccaag gaggagtctg 960
cccactgggt caccacacag tctactgct tctgaagccc gcactgccac cgctcctgcc 1020
ccagaagggt gtttagtttc cacgtaggca ggtcgctttg tgcctctgag tgcgctgctg 1080
tgtgttctct ctatagttct gtgtcataaa gctgtcctgg ccagccttca agctgggtgtg 1140
gccactcttg atgtgaggcg tgtcggttcc aggggggaca tgggaggggc tgcacagtgg 1200
cccgaggcca tgcttgcttc cacctgcagg tgcatttggt cctttccatg gccaggaagc 1260
cctgtgggct gcacttttta tgcttgcaat aacaagagac tccagagtcc tcaccggtgc 1320
agagttggca catattaatt aactaaaatt ctaatgatct tgctaccagc aataaatcaa 1380
gtaggccaag tgaaactggg ctttaaaaag gatggatttc aaatacactg tgcccactag 1440
aagcttcgaa gggcctcgtc cctctgctac agccctggga ggagccagga tccttggttg 1500
tctagctaaa tactgttagg ggagtggtgc ccatctcatc atttcgaaga tagcagagtc 1560
atagttgggc acccggtgat tgggttcaaa aataaagctg gtctgcctct tcaaaaaaaa 1620
aaaaaaaaa aaaaaaaaaa

```

1638

006339E-122700

## (2) INFORMATION ON SEQ ID NO. 7:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

cgccctgcgcg ctgagtgcggt gccgctccgc cgaccgaaga ggctggacat gacaccagtg 60
gcataatcacg gccatgggggt ctcagcattc cgctgctgct cgcccctcct cctgcaggcg 120
aaagcaagaa gatgacaggg acggtttgct ggctgaacga gagcaggaag aagccattgc 180
tcagttccca tatgtggaat tcaccgggag agatagcatc acctgtctca cgtgccaggg 240
gacaggctac attccaacag agcaagtaaa tgagttgggt gctttgatcc cacacagtga 300
tcagagattg cgccctcagc gaactaagca atatgtcctc ctgtccatcc tgctttgtct 360
cctggcatct gggttggtgg ttttcttctt gtttccgcac tcagtccttg tggatgatga 420
cggcatcaaa gtggtgaaag tcacatttaa taagcaagac tcccttgtaa ttctcaccat 480
catggccacc ctgaaaatca ggaactccaa cttctacacg gtggcagtga ccagcctgtc 540
cagccagatt cagtacatga acacagtggg gaattttacc ggggaaggccg agatgggagg 600
accgttttcc tatgtgtact tcttctgcac ggtacctgag atcctggtgc acaacatagt 660
gatcttcatg cgaacttcag tgaagatttc atacattggc ctcatgaccc agagctcctt 720
ggagacacat cactatgtgg attgtggagg aaattccaca gctatttaac aactgctatt 780
ggttcttcca cacagcgccg gtagaagaga gcacagcata tgttcccaag gcctgagttc 840
tgggacctac cccacagtgg gtgttaaggc agagggaagg aattggttca ctttaacttc 900
ccaggcaaac attcctcctg gccacttagg gagggaaaca ccttccctat gggttaccat 960
ttgttgtttg ttcaggaacc aggcggattc agttgcctag gcgtgttgcc ccagcaatta 1020
gtttgggcac tgca
1034

```

## (2) INFORMATION ON SEQ ID NO. 8:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 947 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

09673395-12700



(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

cgaggccctg gcatgtgcaa agagtactga gtgggattcc cagcaggata ccatcaagta 60
ctacaccatg cacctgacca cattgtgcaa cacgtgattg gacaacccaa cccagagaaa120
caaggatcag ctgatccggg cagccgtgaa gtttctggac accgacacca tctgctacag180
ggtggaggag cccgagacat tagtggaact tcaaaggaat gagtgggatc caatcatcga240
atgggctgag aaaagatacg gcgtggagat cagctcctcc accagcataa tgggaccag300
catccctgcc aaaactcggg aggtgctcgt cagccacctg gcatcttaca acacatgggc360
tttacaaggg attgagtttg tagctgcca gctcaagtcc atgggtgctaa ccttgggcct420
gattgacctg cgcctgacag tggagcaggc cgtgctgctg tcacgcctgg aggaggagta480
ccagatccag aagtggggca acattgagtg ggcccatgac tatgagctgc aggagctgcg540
ggcccgacc gccgcggca cctcttcat ccatctctgc tccgagagca ccacagtcaa600
gcacaagctc ctgaaggagt gaggcctggg cagagcacac tcagcaggat agaggcagt660
cagccacagc tccccggcc ttcagggtc cccagcctgt ggggctggct tccttggtt720
ttggggactc ggcctcagcg tcaccctgag attcccccg agacacagtg cgctagtacg780
gctgtccgga ggtcagcctg atttcaaccc aggtgcccct ggcctggcca gcagtgaatg840
taggagatga attgtgcaag tgactttctc tcgactctga ttttattaaa tatttctcca900
ccctggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 947

```

(2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 497 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

09673395.12700

- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
ctcgtggcga gagactgaga taaaagagca actcactgaa caccttttga cgatcataca 60
gcaaaatgag ctccgaaagg ccaagaagtt ggaggagttg atgcaacaac tagatgtaga120
agccgatgaa gagacttttg agcttgaggt ggaggtcgag agattgctac acgaacaaga180
agtagaatca aggagaccag tggttcgttt agagaggcca tttcagcctg cggaggagag240
tgtgacatta gaatttgcta aagagaacag aaagtgtcaa gaacaagctg tttcccaaaa300
ggtagatgac cagtgtggaa attccagtag catccccctt cttagtccaa actgccccaa360
tcaagaaggt aatgacattt cagctgcttt ggccacatga agttctggta ttcttttgag420
ctaataatggt attgagtaaa gtatactttt tgcagtagat catgccctga cctccaataa480
aaacctcttt aaaacaa                                497
```

- (2) INFORMATION ON SEQ ID NO. 10:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 269 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual  
 ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
cggggagagg tgggctgggc tgcaggctct ggcgttgtgc tggatcatcg cgcccgact 60
ctgaagtttt ctccgtggcg ctccctgaga ggggttcctc ctgcatcttg agaataatttt120
gcatttcggc tcccttctct tctcgctgcc atcggatgcc ccaaataagg cctgtcccct180
cgggtgaatca gacttcggaa accgcctcgc ttcaggggtca gagtccaagt acagatgagc240
ttgagaggga ttctgaaatg caacggccc                                269
```

- (2) INFORMATION ON SEQ ID NO. 11:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1717 base pairs

004227 5624960

(B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

attctaggac caacactcct gtggagacgt ggaaagggttc caaaggcaaa cagtcctata 60
cctacatcat tgaggagaac actaccacga gcttcacctg ggccttcacag aggaccactt 120
ttcatgagga aagcaggaag tacaccaatg acgttgccaa gatctactcc atcaatgtca 180
ccaatgttat gaatggcgtg gcctcctact gccgtccctg tgccctagaa gcctctgatg 240
tgggctctct ctgcacctct tgtcctgctg gttactatat tgaccgagat tcaggaaacct 300
gccactcctg cccccctaac acaattctga aagcccacca gccttatggg gtccaggcct 360
gtgtgccctg tgggtccagg accaagaaca acaagatcca ctctctgtgc tacaatgatt 420
gcaccttctc acgcaacact ccaaccagga ctttcaacta caacttctcc gctttggcaa 480
acaccgtcac tcttgctgga gggccaagct tcacttccaa aggggttgaaa tacttccatc 540
actttaccct cagtctctgt ggaaaccagg gtaggaaaaat gtctgtgtgc accgacaatg 600
tcactgacct coggattcct gaggtgagt cagggttctc caaatctatc acagcctacg 660
tctgccagga agtcatcatc cccccagagg tgacaggcta caaggccggg gtttctcac 720
agcctgtcag ccttgctgat cgacttattg gggtgacaac agatatgact ctggatggaa 780
tcacctcccc agctgaactt ttccacctgg agtccttggg aataccggac gtgatcttct 840
tttataggta caatgatgtg acccagtcct gcagttctgg gagatcaacc accatccgcg 900
tcagggtcag tccacagaaa actgtccctg gaagtttgct gctgccagga acgtgctcag 960
atgggacctg tgatggctgc aacttccact tcctgtggga gagcgcggt gcttgcccgc 1020
tctgctcagt ggctgactac catgctatcg tcagcagctg tgtggctggg atccagaaga 1080
ctacttacgt gtggcgagaa cccaagctat gctctggtgg catttctctg cctgagcaga 1140
gagtcacat ctgcaaaacc atagatttct ggctgaaagt gggcatctct gcaggcacct 1200
gtactgccat cctgctcacc gtcttgacct gctacttttg gaaaaagaat caaaaactag 1260
agtacaagta ctccaagctg gtgatgaatg ctactctcaa ggactgtgac ctgccagcag 1320
ctgacagctg cgccatcatg gaaggcgagg atgtagagga cgacctcatc tttaccagca 1380
agaagtcact ctttgggaag atcaaatcat ttacctcaa gaggactcct gatggatttg 1440
actcagtgcc gctgaagaca tcctcaggag gccagacat ggacctgtga gaggcactgc 1500
ctgcctcacc tgctctctca ccttgcatag cacctttgca agcctgcggc gatattgggt 1560
ccagcatcct gcaacaccca ctgctggaaa tctcttcatt gtggccttat cagatgtttg 1620
aatttcagat ctttttttat agagtaccca aacctcctt tctgcttgcc tcaaacctgc 1680
caaataatac cacactttgt ttgtaaatta aaaaaaa

```

1717

004227-5662960

## (2) INFORMATION ON SEQ ID NO. 12:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1419 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

ggcagaggta ttacctgaaa acttaaaaaga aggcctgaag gaatcttcct ggagttcatt 60
accatgtact aaaaacagac cttttgattt tcattcagtg atggaagagt ctcaagtctct 120
caatgaacct agcccaaagc agagtgaaga aataccagag gtcacttcag agcctgtcaa 180
aggaagctta aaccgtgctc agtcagcaca gtctataaat tcaacagaaa tgcctgccag 240
agaggactgt ttgaaaaaag agtgccctca gaacctgttc tgtcagttca agaaaaagg 300
gttctgctga aaagaaagtt gtctctttta gaacaggatg tgattgtaaa tgaagatgga 360
agaaataagc tgaaaaaaca aggagaaact cccaatgaag tctgtatgtt ttccttagct 420
tatggtgata ttccagaaga attaatcgat gtctcagatt tgcagtgttc tctctgcatg 480
aggttgtttt ttgagccagt aacaaccctt tgcggacatt cgttctgtta gaattgtctt 540
gagcgttggt tagatcatgc accatattgt cctctttgca aagaaagctt aaaagagtat 600
ctagcagata ggaggtactg tgtcacacag ctgttggaag gaattaatag tgaagtatct 660
gcctgatgaa ctgtctgaga gaaaaaaaaa atatgatgaa gaaactgctg aactctcaca 720
cttgaccaag aatgttccaa ttttgtttg cactatggcc taccctactg tgccttgccc 780
tctccatgta tttgagccaa gatacagatt gatgattcga agaagtatac agactggaac 840
caaacagttt ggcatgtgtg tcagtgtatc acaaaatagt tttgcagatt atggttgat 900
gttacaaatt agaaacgtgc atttcttacc ggacggaagg tctgtggttg atacagttgg 960
aggaaagcgg tttagggttt taaaaagagg aatgaaagat ggatattgca ctgccgacat 1020
tgaatatctg gaagatgtta aggttgagaa tgaagatgag attaagaatc tcagagagct 1080
tcatgatttg gtttactctc aagcctgcag ctggtttcag aatttaagag acagatttcg 1140
aagccaaatt cttcagcatt tcggatcaat gcccgagagg agggaaaacc ttcaggcagc 1200
ccctaattga cctgcattgg tttggtggct tcttgagtt ctccctgtag acccagcata 1260
ccagctgtcg gttttgtcaa tgaagtcttt gaaagaacgg ttgaccaaga tacagcatat 1320
actgacctat ttttctagag accaattcta agtaactaac tctttgggat cttccctttg 1380
aaagttgacc cctaattctt gggctgccat ttggttggg 1419

```

09673395 12700

## (2) INFORMATION ON SEQ ID NO. 13:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 671 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

agcgcggtga agcggggggtg ggatctgaac atggcgggcg tggtagctgc tacggcgctg 60
aagggccggg gggcgagaaa tgccgcgctc ctccggggga ttctcgagg agccacagct120
aacaaggctt ctcataacag gacccggggc ctgcaaagcc acagctcccc agagggcaag180
gaggaacctg aacccctatc cccggagctg gaatacattc ccagaaagag gggcaagaac240
cccatgaaaag ctgtgggact ggcctggggc atcggttcc cttgtggtat cctcctcttc300
atcctcacca agcgggaagt ggacaaggac cgtgtgaagc agatgaaggc tcggcagaac360
atgcggttgt ccaacacggg cgagtatgag agccagaggt tcagggttc ctcccagagt420
gccccgtccc ctgatgttg gtctgggtg cagacctgag gagcgctgcg accctcctag480
gctattgact gttaagtct caggtttgg ccagattcca gttcgtgcct ctgaggtcca540
ccagagggcg catgaagccc aggctgttg caaacctac cctgccccac accaaggagc600
ccaccaaagg caaataaagt tattgagtgt ttagtagaaa ggaaaaaaaa aaaaaaaaaa660
aaaagtcgac c

```

671

## (2) INFORMATION ON SEQ ID NO. 14:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 524 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

004227 562960

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

aagtgttctc agatgctgat gtttgtaagg tcccgggtggg gccatgagga agaagaggag 60
ctgaaggtaa gagactcata aacaagatga ctctttgatg catgaacaag atttgaaaat120
ctcaagcctg taaagaatac ccctgctatt taaataaagc tcataccaag aggtaacatt180
ttgccccggg ccaaattcag gggcttagtg ccctgcattc ctttgaggca aaaaataaat240
gggctatgac tggttaaatg tccaaaagggt gaattctcat ttcattcaaa caaagacaga300
tttgcgcatc cactcaagca gaatgtggcc atgaatattc agcccctgca tacatacaaa360
gatgtacgca tgattcccc caccaagcac acacacagtc acacacgcac acacacacac420
atgcacacac gcgcgtgcac acacggacac atgcacacac acacgcacac gtaaacacat480
gcacacatgc acacacgtgc acacatgcac acacggacac actt                               524

```

## (2) INFORMATION ON SEQ ID NO. 15:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 345 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

aaactttctt tctacaaaaa atcaaaagct tagctgatag atcatgaaaa tagattatga 60
acagtgaat tctgagaag gctgaaagt cggggaacca aagcagggga gattagcctt120
agtccggagg agggagaagc agatggaagt cagcagcctg ccttgttttt acgtgtaata180
tttaaatatt caaattgtat tacaggagg cctactttct gtttttatca agagtttttc240
ttttgttcaa agacactggt tatgggaata ttttgaaagg gtaagaaacg ctggtataaa300
aaggtgttgc agattaattt tgaaggctct tacggaacca gtccc                               345

```

004221 562960

## (2) INFORMATION ON SEQ ID NO. 16:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

ggcggtccca ggcaggccca gaagctgggc agcctctgcc gggttccggg aaaaggagct 60
cctgctgccA ctgctcttcc ggagcctgca gcatggggcc cctgccgcgc accgtggagc 120
tcttctatga cgtgctgtcc ccctactcct ggctgggctt cgagatcctg tgccgggtatc 180
agaatatctg gaacatcaac ctgcagttgc ggcccagcct cataacaggg atcatgaaag 240
acagtggaaa caagcctcca ggtctgcttc cccgcaaagg actatacatg gcaaatagact 300
taaagctcct gagacaccat ctccagattc ccattccactt ccccaaggat ttcttgtctg 360
tgatgcttga aaaaggaagt ttgtctgcca tgcgtttcct caccgccgtg aacttggagc 420
atccagagat gctggagaaa gcgtcccggg agctgtggat gcgcgtctgg tcaagggaatg 480
aagacatcac cgagccgcag agcatcctgg cggctgcaga gaaggctggt atgtctgcag 540
aacaagccca gggacttctg gaaaagatcg caacgccaaa ggtgaagaac cagctcaagg 600
agaccactga ggcagcctgc agatacggag cctttgggct gcccatcacc gtggcccatg 660
tggtatggcca aaccacatg ttatttggct ctgaccggat ggagctgctg gcgcacctgc 720
tggtgagagaa gtggatgggc cctataacctc cagccgtgaa tgccagactt taagattgcc 780
cggaggaagc aaactcttcg tataaaaaaa gcaggccatc tgcttaacctt ttggctccac 840
cataaggcac tgggactcgg atttctctat ctgatatagg tattttctgt ggccctggga 900
gctgtctgtc tttccctac ccccaaggat gccaggaaga cgtccaccat tagccatgtg 960
gcaaccttta cttctatgcc tcacaagtgc ctttcagaga gcccgaattc tgctttccca 1020
caaaataaac ctaatgccat caggcaaaaa aaaaaaaaaa 1060

```

## (2) INFORMATION ON SEQ ID NO. 17:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1721 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

09673395-122700

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

ctctctctct tctctgtctct tctctgctcc ctctctttct ctctctccctc tgccttccca 60
gtgcataaaag tctctgtctgc tcccggaaact tgttggcaat gcctattttt tggctttccc 120
ccgcgtttctc taaactaact atttaaaggt ctgcggtcgc aaatggtttg actaaacgta 180
ggatgggact taagttgaac ggcagatata tttcactgat cctcgcggtg caaatagcgt 240
atctggtgca ggccgtgaga gcagcgggca agtgcgatgc ggtcttcaag ggcttttcgg 300
actgtttgct caagctgggc gacacatggc caactacccg caggcctgga cgacaagacg 360
aacatcaaga ccgtgtgcac atactgggag gatttccaca gctgcacggt cacagccctt 420
acggattgcc aggaaggggc gaaagatatg tgggataaac tgagaaaaga atccaaaaac 480
ctcaacatcc aaggcagctt attcgaactc tgcggcagcg gcaacggggc ggccgggggtcc 540
ctgctcccg cgttcccggt gctcctggtg tctctctcgg cagcttttagc gacctggctt 600
tccttctgag cgtggggcca gctccccccg cgcgccacc cactcact ccatgctccc 660

ggaaatcgag aggaagatcc attagttctt tggggacggt gtgattctct gtgatgctga 720
aaacactcat ataggattgt gggaaatcct gattctcttt tttatttcgt ttgatttctt 780
gtgttttatt tgccaaatgt taccaatcag tgagcaagca agcacagcca aaatcggacc 840
tcagcttttag tccgtcttca cacacaaata agaaaacggc aaacccaccc cattttttaa 900
ttttattatt attaatTTTT tttgttgga aaagaatctc aggaacggcc ctggggccacc 960
tactatatta atcatgctag taacatgaaa aatgatgggc tctcctaata aggaaggcga1020
ggagaggaga aggccagggg aatgaattca agagagatgt ccacggacga aacatacgg1080
gaataattca cgtcacgctc gttcttccac agtatcttgt tttgatcatt tccactgcac1140
atttctcctc aagaaaagcg aaaggacaga ctgttggtt tgtgtttgga ggataggagg1200
gagagagggg aggggctgag gaaatctctg gggttaagag aaaggcttcc agaagacatg1260
ctgctatggt cactgagggg ttagctttat ctgctgttgt tgatgcatcc gtccaagt1320
actgccttta ttttccctcc tccctcttgt tttagctgtt acacacacag taatacctga1380
atatccaacg gtatagatca caaggggggg atgttaaattg ttaatctaaa atatagcta1440
aaaaagattt tgacataaaa gagccttgat tttaaaaaaa aaagagagag agatgtaatt1500
taaaaagttt attataaatt aaattcagca aaaaagatt tgctacaaag tatagagaag1560
tataaaataa aagttattgt ttgaaaaaaa agtgtcgttt gtttcctacc ccaacctgct1620
ttcttgaccc agttctcagg gaacctgaag ggacacagga tgccgggtgat aagctcacct1680
cttcagggaag ccgcttcaag cagacctgcc accttcaagc a 1721

```

09673395-122700



## (2) INFORMATION ON SEQ ID NO. 18:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2367 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

accctgtggt cccgggtttc tgcagagtct acttcagaag cggaggcact gggagtccgg 60
tttgggattg ccaggctgtg gttgtgagtc tgagcttggt agcggtctgt gcgccccaac 120
tcttcgccag catatcatcc cggcaggcga taaactacat tcagttgagt ctgcaagact 180
gggaggaact ggggtgataa gaaatctatt cactgtcaag gtttattgaa gtcaaaatgt 240
ccaaaaaat cagtggcggg tctgtggtag agatgcaagg agatgaaatg acacgaatca 300
tttgggaatt gattaaagag aaactcattt ttccctacgt ggaattggat ctacatagct 360
atgatttagg catagagaat cgtgatgcca ccaacgacca agtcaccaag gatgctgcag 420
aagctataaa gaagcataat gttggcgtca aatgtgccac tatcactcct gatgagaaga 480
gggttgagga gttcaagttg aaacaaatgt ggaaatcacc aaatggcacc atacgaaata 540
ttctgggttg cacggtcttc agagaagcca ttatctgcaa aaatatcccc cggcttggtga 600
gtggatgggt aaaacctatc atcataggtc gtcattgctt tggggatcaa tacagagcaa 660
ctgattttgt tgttctctgg cctggaaaag tagagataac ctacacacca agtgacggaa 720
cccaaaaggt gacatacctg gtacataact ttgaagaagg tgggtggtgt gccatgggga 780
tgtataatca aqataaqtca attgaagatt ttqcacacag ttcccttcaa atqactctgt 840

ctaagggttg gcctttgtat ctgagcacca aaaacactat tctgaagaaa tatgatgggc 900
gttttaaaaga catctttcag gagatatatg acaagcagta caagtcaccag tttgaagctc 960
aaaagatctg gtatgagcat aggtcctatc acgacatggt ggcccaagct atgaaatcag1020
agggaggctt catctgggcc tgtaaaaaat atgatggtga cgtgcagtcg gactctgtgg1080
cccaagggtg ttggtctctc ggcatgatga ccagcgtgct ggtttgtcca gatggcaag1140
cagtagaagc agagggtgcc cacgggactg taacccgtca ctaccgcatg taccagaaag1200
gacaggagac gtccaccaat cccattgctt ccatttttgc ctggaccaga ggggttagccc1260
acagagcaaa gcttgataac aataaagagc ttgccttctt tgcaaatgct ttggaagaag1320
tctctattga gacaattgag gctggcttca tgaccaagga cttggctgct tgcaattaaag1380
gtttacccaa tgtgcaacgt tctgactact tgaatacatt tgagttcatg gataaacttg1440
gagaaaactt gaagatcaaa ctagctcagg ccaaacttta agttcatacc tgagctaag1500
aggataattg tcttttggtg actaggtcta cagggtttaca tttttctgtg ttacactcaal560
ggataaaggc aaaatcaatt ttgtaatttg tttagaagcc agagtttatc ttttctataal620
gtttacagcc tttttcttat atatacagtt attgccacct ttgtgaacat ggcaagggacl680
ttttttacaa tttttatttt attttctagt accagcctag gaattcggtt agtactcatt1740
tgtattcact gtcacttttt ctcatgttct aattataaat gaccaaatac aagattgctcl800
aaaagggtaa atgatagcca cagtattgct ccctaaaata tgcataaagt agaaattcac1860
tgccttcccc tctgtccat gaccttgggc acagggaagt tctggtgtca tagatatccc1920
gttttgtgag gtagagctgt gcattaaact tgcacatgac tggaacgaag tatgagtgc1980
actcaaagt gttgaagata ctgcagtcct ttttgtaaaag accttgctga atgtttccaa2040
tagactaaat actgttttag ccgcaggaga gtttggaatc cggaataaat actacctgga2100
ggtttgtcct ctccattttt ctctttctcc tcttgacctg gcctgaatat tatactactc2160
taaatagcat atttcattcc agtgcaataa tttgaagctg atcttttttg gacttctgct2220
ggcctgtttt atttctttta tataaatgtg atttctcaga aattgatatt aaacactatc2280
ttatcttctc ctgaactgtt gattttaatt aaaattaagt gctaattacc attaaaaaaa2340
aaaaaaaaa aaaaaaaaaa aaaaaaa

```

2367

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 19:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1321 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

cctggaaca agatccaaac ccaagtgacc ccgccgaaa gtgacccagt cagggtttaa 60
aattccaaca aaccgacgtg aacaaataga ccgaccaacc aaatatacaa tccgtcaaaa 120
tacattcact tccactacga aaccccaaca aagggtgtga atgcccgccc aggagagacg 180
gttttggtt catcaagtgt gtggatcgtg atgttcgtat gttcttcac ttcagtga 240
ttctggatgg gaaccagctc catattgcag atgaagtaga gtttactgtg gttcctgata 300
tgctctctgc tcaaagaaat catgctatta ggattaaaaa acttcccaag ggcacggtt 360

catttcattc ccattcagat caccgttttc tgggcacggt agaaaaagaa gccacttttt 420
ccaatcctaa aaccactagc ccaaataaag gcaaagagaa ggaggctgag gatggcatta 480
ttgcttatga tgactgtggg gtgaaactga ctattgcttt tcaagccaag gatgtggaag 540
gatctacttc tctcaataa ggagataagg ttgaatttag tattagtga aaacagaggg 600
ctggacagca ggttgcaact tgtgtgcgac ttttaggtcg taattctaac tccaagaggg 660
tcttggttta tgtggcaact ctgaaggata attttggtt tattgaaaca gccaatcatg 720
ataaggaaat ctttttccat tacagtgaat tctctggtga tgttgatagc ctggaactgg 780
gggacatggt cgagtatagc ttgtccaaag gcaaaggcaa caaagtcagt gcagaaaaag 840
tgaacaaaac acactcagtg aatggcatta ctgaggaagc tgatcccacc atttactctg 900
gcaaagtaat tcgccccctg aggagtgtt atccaacaca gactgagtac caaggaatga 960
ttgagattgt ggaggagggc gatatgaaag gtgagggtcta tccatttggc atcgttggga 1020
tggccaacaa aggggattgc ctgcagaaa gggagagcgt caagttccaa ttgtgtgtcc 1080
tgggccaacaa tgcacaaact atggcttaca acatcacacc cctgcgcagg gccacagtgg 1140
aatgtgtgaa agatcagttt ggcttcatta actatgaagt aggagatagc aagaagctct 1200
ttttccatgt gaaagaagtt caggatggca ttgagctaca ggcaggagat gaggtggagt 1260
tctcagtgat tcttaagagt tcaggcggac tggcagggtc aggcgcctgt agatgttttg 1320
g
1321

```

09673395-12700

## (2) INFORMATION ON SEQ ID NO. 20:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 384 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

ggtcgaatcc aaatcactca ttgtgaaagc tgagctcaca gccgaataag ccaccatgag 60
gctgtcagtg tgtctcctga tggctcgcgt ggccctttgc tgctaccagg cccatgctct120
tgtctgcccc gctgttgctt ctgagatcac agtcttctta ttcttaagtg acgctgcggt180
aaacctccaa gttgccaaac ttaatccacc tccagaagct cttgcagcca agttggaagt240
gaagcactgc accgatcaga tatcttttaa gaaacggctt ctcatttgaa aaagtcctgg300
gtgggaatag tgaaaaaatg tgggtgtgtg acatgtaaaa atgctcaacc tgggtttcca360
aagtcttttc aacggcaacc tgat                                     384

```

## (2) INFORMATION ON SEQ ID NO. 21:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 367 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

004227 55554960

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

gggcactggt ggtccggttc ctcaccaaac gattcatcgg tgactatgaa agaaatgcag 60
gtaatctcta tactagacaa gttcagatag aagggtgaaac cctggctctt caggttcaag120
acaactccagg tattcagggtc catgagaaca gcctgagctg cagtgaacag ctgaataggt180
gcattcgctg ggcagatgct gtggtgatcg ttttctccat cactgactac aagagctatg240
aactcatcag ccagctccac cagcacgtgc agcagctaca ccttgggcac ccggctgcct300
gtgggtgggc gtggggccaac aaaagtgacc tgttgacat caaacagggt gaccctcagc360
ttggact

```

(2) INFORMATION ON SEQ ID NO. 22:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2621 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

004227" 5622960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

gggcctttgc ccgccttggc ggccggctct acgttccttg ttctcgctg cagctccgcc 60
atggctccta aaggcagctc caaacagcag tctgaggagg acctgctcct gcaggatttc 120
agccgcaatc tctcgcccaa gtccctccgc ctcttcttcg gaaacgcgtt catcgtgtct 180
gccatcccca tctggttata ctggcgataa tggcatatgg atcttattca gtctgctgtt 240
ttgtatagtg tgatgacctt agtaagcaca tatttggtag cctttgcata caagaatgtg 300
aaatttgttc tcaagcacia agtagcacag aagagggagg atgctgtttc caaagaagtg 360
actcgaaaaa tttctgaagc tgataataga aagatgtctc ggaaggagaa agatgaaaga 420
atcttgtgga agaagaatga agttgctgat tatgaagcta caacattttc catcttctat 480
aacaacactc tgttcctggg cgtggtcatt gttgcttctt tcttcatatt gaagaacttc 540
aaccaccacg tgaactacat attgtccata agtgcttcat caggactcat cgccctcctg 600
tctactggct ccaaatagac catgtcagct tcacccctcg gctttgtgtc tatgggtggc 660
ctgtggtata tggaaaagta gcagggtggg cagggtggga gacacaagat gtttttatag 720
tctagagcct ttaaaaaacc cagcagaatg taattcagta tttgtttatt ggctgttttt 780
tgacagattg ttgaaattaa atgaattgaa agggaaactc agagtactag gacgtttatt 840
aaaaggaaaa aaatgtcttg caatgtgctg taatcacaaaggagaaaaa aacttgtttc 900
cttgatctgt cagaggtcac agtaacctgg gccgagctgt tattatttat tatataatag 960
tagtaggaag ttaataactg gttctctgtg ttccaagcac aatattacaa cttcttttgat 1020
accgtaataa tcagaatgaa tctctctccc aggggattga acagaagctt aatgtttaca 1080
agtgtttgaa tttgtgatct gaaataaacac aaaattaaaa acatgatttc tctaattttc 1140
caactagagg aagagaaact tgtggaaaag ttcttttttt ttcgtttttt tttcttaaaag 1200
aagggcagcc aaggtagtaa cctaaaaata gtgccaggc atatgagagt tgcctacgal 1260
ggttaaagaa cacactgttc cactgtatgg ctttggccct gagtggccag ggaggtcaac 1320
ttgaccctgc catgttggtt tgacttacta agacacagga atcattgttt tcttgaccal 1380
gggtctcaca ccctggagga atgttaaagta agagaaaagaa cctctttcct gaatttgac 1440
atgtaaaaa ccaaagtaat ttttctgaac ttctgcaatt ctgagaactc tccaaggaat 1500
ttacagtgat tttagtgtt gtcagcattt ttccatgagg actttcatal atttgactct 1560
ttagttcaca ggttcccatt gattgtgagc aagatattta tctctttagc cttgggggat 1620
ccagctgaga gcaatctctt gcattttttt acccgtgtat gtacagatat cattcttgt 1680
gtatgccatg acttgaaaaa gtttgggaag ctcttttagca atatcagcta aaaggatat 1740
aaatcacagg tgatagcagt tgtcattcag taatttccta caagcagcac ccaaaggaa 1800
atatagtcct aatctttact atccacttct aaatttaatg tgaatttcac acatgtttat 1860
agttgttttc tttataattt tataaaaaatt attcatcggg agtttaactt ccacttccat 1920
gctatcggat gtgttgggct ccatgcaaga acttggaaaga aaaacaggca ggaatgcatt 1980
tgcataatga cccagatcat cattttctgc aactgagaat tatatttcac cattgcttct 2040
agaagtctgc aattctttac ttttcttttg tgcatatta tctaggtgcc atcactggat 2100
aatgtggagt gactagagaa gtcacatata actgtaaggt acagttaggg taacacttta 2160
gaggtttatt atttttaaaa aacttttctt gaactcctgg ccaacatggg gaaaccccg 2220
ctctactaaa aataccaaaa ttagccaggc gtgatgggtg gtgcctgtaa tctcagctac 2280
ttgggaggct gaagcaggag aactgcctga acccaggagg cagaggttgc agtgagtcga 2340
gatcgtgcta ctactgcctg ggtggcaagg gtgagactcc atctcaaaaa agaaacaaaa 2400
aaacccaaaa agttttcttt actgttggtt aaaaaaaaaa gccagaccat agtttgactg 2460
gtggcatgga atttgtgtat caaataaatg catttgctta tttgacaaac aaaaagtgtc 2520
cactattggt gaccgaggtg gggccgtttt tttgaaattg ggggggaaat ttgcccggtg 2580
gtgggagggc ctttgtgggg ggggaaaaat tgcccccttg g 2621

```

09673395-12200

## (2) INFORMATION ON SEQ ID NO. 23:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2019 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

ctgtatoccta atttcttgggt gaatgaactc attctttaaagc agaagcaaag atttgaggaa 60
aagagggttca aattggacca ctccagtgaat agcaccaatg gccacagggtg gcagatattt 120
caagattgggt tgggaactga ccaagataac ctctgatttgg ccaatgtcaa tcttatgttg 180
gagttactag tgcagaagaa gaaacaactg gaagcagaat cacatgcagc ccaactacag 240
attcttatgg aattcctcaa ggttgcaaga agaaataaga gagagcaact ggaacagatc 300
cagaaggagc taagtgtttt ggaagaggat attaagagag tgggaagaaat gagtggctta 360
tactctcttg tcagtggagg tagcacagtg cctcaatttg aagctccttc tccatcacac 420
agtagtatta ttgattccac agaatacagc caacctccag gtttcagtgg cagttctcag 480
acaaagaaac agccttggtg taatagcacg ttagcatcaa gacgaaaacg acttactgct 540
cattttgaag acttgagcga gtgttacttt tctacaagga tgtctcgtat ctccagatgac 600
agtcgaactg caagccagtt ggatgaattt caggaatgct tgtccaagtt tactcgatat 660
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atagtctcta gtattgaatt tgaccgggat tgtgactatt ttgcgattgc tggagttaca 780
aagaagatta aagtctatga atatgacact gtcatccagg atgcagtggg tattcattac 840
cctgagaatg aaatgacctg caattcgaaa atcagctgta tcagttggag tagttaccat 900
aagaacctgt tagctagcag tgattatgaa ggcactgtta ttttatggga tggattcaca 960
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taactccatg gacattgctg ctcttggtgg ttttatctaa tttttgtgat agggaaacaa1920
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aaaaaaaaaa aaaaaagaaa agaagggagg agggaaagg 2019

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00673395-122700

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

gtgggtgctg	tgacaggcac	tatttgaagt	gctttatcat	ggattaactc	ttaatcctca	60
gctaccggtat	aaagtaggac	ataaccccat	ttcacatgca	ctacactgag	acttgccctcc	120
tctcccccca	cattgaagat	gttctttttt	cataactata	tactattcca	ttgcatgaat	180
attctgtaat	ttattttaatc	ccctatggat	tgataattag	gttcattata	gatagaagtg	240
taattaacat	tcctgtacat	gtatttttgc	acttgtgtgg	gtattttctgt	aggatgaata	300
actagaaaat	tattggatca	ggtttcacat	ttgcagtttt	gaaaactact	acaaaaaaga	360
tttcagaaat	ttacaacctc	atcattagta	agaatgcctg	tttgccata	gtctgccaac	420
cctgaatcct	taaaaatttt	tgccaatctg	gtaggcaaaa	tttctttctt	ttctttgaat	480
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gcttttgccc	attttccctt	ttttaattat	gaaagtctaa	tgactacctt	ctcattgtat	600
aaaaaacaca	gttctttgaa	tagagagacc	cttttctcca	atgctaccaa	tcacattcca	660
cttaccacag	tttaacatac	atcctctagt	cacctttccg	tacgaatata	catacacata	720
aaaaacattt	ttacataaat	aggatctcat	attctgtagc	tttttaaaat	tttgggtctca	780
aaaaaagtt	acaggtcttt	aaattttctt	aatggttgaa	tatgattaaa	tactatgaaa	840
atgccattat	ttattccctt	aatttttttt	ctctcgctat	tacatttgca	aagtaaacat	900
cctattcaga	tgtctttgtg	catgtgtgtg	aatatttctt	tagtctggag	tccagtaagg	960
tggatttttg	gatcaaaggg	tttgttctct	gtccaccttc	agtcttccca	aaggccttcac	1020
taactgtatt	ttcaccaagt	gtatggagaa	tgttcatttc	cccatataac	catacctacac	1080
cttgatagtt	tttatctggt	gggcgaaaaa	gaaccttttc	ttatttttgc	tttccctgat	1140
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tgctagcaga	aatggaaaga	gaactaagtt	ctgatgtcat	ttttctggag	gccctagatc	1620
cagctgtgcc	taaagcctgc	cctacctccg	gactttaaag	ttttgtgagc	caataaagtc	1680
cctttctttgt	ttaagataat	tgaattgagt	ttctgttctg	attaatatag	gttattttgt	1740
ttttctttatt	gatttgtaga	aaacctttgt	aatttttaa	tctagacttt	atgcactata	1800
taagttaata	aaattagcat	ggccttccat	gaaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa	1860
aaaaaa						1860

## (2) INFORMATION ON SEQ ID NO. 25:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1189 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

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ctagcaagca ggtaaacgag ctttgtacaa acacacacag accaacacat cccgggatgg 60
ctgtgtgttg ctagagcaga ggctgattaa acactcagtg tgttggctct ctgtgccact 120
cctggaaaat aatgaattgg gtaaggaaca gttaataaga aaatgtgcct tgctaactgt 180
gcacattaca acaaagagct ggcagctcct gaaggaaaag ggcttgtgcc gctgccgttc 240
aaacttgtca gtcaactcat gccagcagcc tcagcgtctg cctccccagc acaccctcat 300
tacatgtgtc tgtctggcct gatctgtgca tctgctcgga gacgctcctg acaagtccgg 360
aatttctcta tttctccact ggtgcaaaga gcggatttct ccctgcttct cttctgtcac 420
ccccgctcct ctcccccagg aggctccttg atttatggta gctttggact tgcttccccg 480
tctgactgtc cttgacttct agaatggaag aagctgagct ggtgaaggga agactccagg 540
ccatcacaga taaaagaaaa atacaggaag aaatctcaca gaagcgtctg aaaatagagg 600
aagacaaaact aaagcaccag catttgaaga aaaaggcctt gagggagaaa tggcttctag 660
atggaatcag cagcggaaaa gaacaggaag agatgaagaa gcaaaatcaa caagaccagc 720
accagatcca ggttctagaa caaagtatcc tcaggcttga gaaagagatc caagatcttg 780
aaaaagctga actgcaaatc tcaacgaagg aagaggccat tttaaagaaa ctaaagtcaa 840
ttgagcggac aacagaagac attataagat ctgtgaaagt ggaaagagaa gaaagagcag 900
aagagtcaat tgaggacatc tatgctaata tccctgacct tccaaagtcc tacatacctt 960
ctagggttaag gaaggagata aatgaggaaa aagaagatga tgaacaaaat aggaaagctt 1020
tatatgccat ggaaattaaa gttgaaaaag acttgaggac tggagaaaag acagttctgt 1080
cttcaatacc tctgccatca gatgacttta aaagggtccag gagtaaaagt ttatgatgat 1140
gggcaaaaagt ccagtgtatt cagtaaagtg ctaatcacia gttggagggt 1189

```

## (2) INFORMATION ON SEQ ID NO. 26:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

00673395-122700



(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

gagctcgag ctccgcccgc gcctggtccc agcgcccgcg ggcgcccgtc cccggcccaa 60
ccatggcgctc ctccgcccgc ggcctggtgg tgatcggttg cagtggagtc attgggcgaa 120
gtgggccatg ctgtttgccg gtggaggctt ccagggtgaaa ctctatgaca ttgagcaaca 180
gcagataagg aacgcccctg aaaacatcag aaaggagatg aagttgctgg agcaggcagg 240
ttctctgaaa ggctcccctg gtgtggaaga gcagctgtca ctcatcagtg gttgtcccaa 300
tatccaagaa gcagtagagg gtgccatgca cattcaggaa tgtgttccag aagatctaga 360
actgaagaag aagatttttg ctcatgttaga ttccatcatt gatgatcgag tgatcttaag 420
cagttccact tcttgtctca tgccttccaa gttgtttgct ggcttgggtc atgtgaagca 480
atgcatcgct gctcatcctg tgaatccgcc atactacatc ccgctggttg agctgggtccc 540
ccaccggag acggccccta cgacagtggc cagaacccac gccctgatga agaagattgg 600
acagtgcctc atgagagtc agaaggaggt ggccggcttc gttctgaacc gcctgcaata 660
tgcaatcatc agcgaggcct ggccgctagt ggagggaagg atcgtgtctc ctagtacact 720
ggaccttgtc atgtcagaag ggttgggcat gcggtatgca ttcattggac ccctggaaac 780
catgcatctc aatgcagaag gtatgttaag ctactgcgac agatacagcg aaggcataaa 840
acatgtccta cagacttttg gacccattcc agagttttcc agggccactg ctgagaagg 900
taaccaggac atgtgcatga aggtccctga tgaccgggag cacttagctg ccaggaggca 960
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aatttcttgt aatgcagctt ccactcctct cattggaggc cctatttggg aacactgcaal 1080
gcccttaatc agccctctgt gacataggtg gcagcccacg gagatcctaa gctggctgtcl 1140
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gccctgggac tggcggcaca gcagcacttg cgttctcggt gctgtcgatt tcctgccacc 1260
tgggcagata acctggagat ttccacctt tctttttcag cttgattgca tttgagtatg 1320
atttgacagc cagtgattgt agttttcatg ttaatatgtg ggcaaaatat ttttgaatt 1380
atttttgtaa tccctttctg agtaatctgg gggtcctt 1418

```

(2) INFORMATION ON SEQ ID NO. 27:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 814 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

004227 6622960

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

gcagcaacgg ggtgcggcag ggtggggaac gcgggagggg gccagctccc aggaaagctg 60  
gtctgcgagc ggccccctgcc cggctcccag gtccctgcgc gacccccgcc ttcccagac120

cccagccggg ctgccgcccg cgtcccggaa gctccagcct gaaccatggt tttcacttgt180  
ggcccaaagt aggcacatgt ggtctccggg ttctgccgaa gccccccagt catggtggct240  
ggagggcggtg tctttgtcct gccctgcac caacagatcc agaggatctc tctcaacaca300  
ctgacctca atgtcaagag tgaagaggtt tacactcgcc atgggggtccc catctcagtc360  
actggcattg cccaggtgaa gctttcagag ccttttcccc acagtccact tccccatcac420  
cctctctccc agacattaag acatcttctg gccacagtct tctcaaccct tgccctgcaga480  
gaagttccctc tgctagtctc atcttttcca ggcaccccaa ggcacttgcc tctcctcct540  
ttctttccct gaaatggaag aagcatttct gagagggctc tcccttctct ctctgctttt600  
cctctgactt catgagacct ccaccacacc tttctacct ctactctggc tacaggtaaa660  
aatccagggg cagaacaagg agatgttggc ggccgcctgt cagatgttgc tggggaagac720  
ggaggttgag attgccaca ttgccctgga gacgttagag ggccaccaga gggccatcat780  
ggccacatg acttgtggga ggggtgggct taga 814

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 3039 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

09673395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

gaactgagat	attgtaatca	aatagttaac	atcaggaagt	taatttggct	ggcaaaattc	60
tagggaaaact	tggccagaaa	actggtggtg	aaggcttttg	ctcatataaa	caagtgccat	120
tgagtttcaa	atgaccagca	aatatatatta	gaacccttcc	tgtttttatgt	ctgtacctcg	180
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gtggccctac	tgactggtaa	tggttagagg	catttatgga	ttttaagctt	tgaggaaaaa	480
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catttgaggg	ataccaggg	agtcttgggt	gttccttctc	tggggaagca	aacatttcac	1140
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tgagggtaaa	tggagaaaaa	atcttctggg	ttacaatgaa	tgtaagccca	aattgtggaa	2040
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tcgtgaaaag	aattactata	aggtactgtg	aaataactgc	gattttgtga	gcaaaaacata	2940
cttggaatg	ctgattgatt	tttatgcttg	ttagtgtatt	gcaagaaaca	cagaaaatgt	3000
agttttgttt	taataaacca	aaaattgaac	ataaaaacc			3039

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 29:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

taccaatctg aagggggaag cggcgccgcc atcgccctccc ggcgctccct ccccgactcc 60
taagtccttc ggccgccacc atgtccgcct cggctgtctt cattctggac gtttaagggca 120
agccattgat cagccgcaac tacaagggcg atgtggccat gagcaagatt gagcacttca 180
tgcctttgct ggtacacggg gaggaggaag gcgccctggc cccgctgctg agccacggcc 240
agggccactt cctatggatc aaacacagca acctctactt ggtggccacc acatcgaaga 300
atgccaatgc ctccctgggtg tactccttcc tgtataagac aatagaggta ttctgcgaat 360
acttcaagga gctggaggag gagagcatcc gggacaactt tgtcatcgtc tacgagttgc 420
tggacgagct catggacttt ggcttccgcg agaccaccga cagcaagatc ctgcaggagt 480
acatcactca gcagagcaac aagctggaga cgggcaagtc acgggtgccca cccactgtca 540
ccaacgctgt gtcctggcgc tccgagggta tcaagtataa gaagaacgag gtcttcattg 600
atgtcataga gtctgtcaac ctgctgggtca atgccaacgg cagcgtcctt ctgagcgaaa 660
tcgtcgggtac catcaagctc aaggtgtttc tgtcaggaat gccagagctg cggctggggc 720
tcaatgaccg cgtgctcttc gagctcactg gcgcgagcaa gaacaaatca gtagagctgg 780
aggatgtaaa attccaccag tgcgtgcggc tctctcgctt tgacaacgac cgcaccatct 840
ccttcatccc gcctgatggt gactttgagc tcatgtcata ccgcctcagc acccaggtca 900
agccactgat ctggattgag tctgtcattg agaagttctc ccacagccgc gtggagatca 960
tgggtcaaggc caaggggcag tttaagaaac agtcagtggc caacgggtgtg gagatatctg 1020
tgcctgtacc cagcgatgcc gactccccca gattcaagac cagtgtgggc agcgccaagt 1080
atgtgccgga gagaaacgtc gtgatttgga gtattaagtc tttcccgggg ggcaaggagt 1140
acttgatgcg agcccacttt ggcctccccca gtgtggaaaa ggaagagggtg gagggccggc 1200
cccccatcgg ggtcaagttt gagatcccct acttcaccgt ctctgggatc caggtccgat 1260
acatgaagat cattgagaaa agtggttacc agggccctgc cctgggggtt cgctacattc 1320
acccagagtg ggcgattacc aactttcggt accagctagg aaggggagaa gagatggggg 1380
ggttttaaca cggggtttgc ttacagccc cggtatgcaga tttttagaag ggagggcagg 1440
tgcgggtt
1448

```

002221 5652960

## (2) INFORMATION ON SEQ ID NO. 30:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1394 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```
atgaatacaa ggctgcaagt ggaacatcct gttactgaga tgatcacagg aactgacttg 60
gtggagtggc agcttagaat tgcagcagga gagaagattc ctttgagcca ggaagaaata 120
actctgcagg gccatgcctt cgaagctaga atatatgcag aagatcctag caataacttc 180
atgcctgtgg caggcccatt agtgcacctc tctactcctc gagcagaccc ttccaccagg 240
attgaaactg gagtacggca aggagacgaa gtttccgtgc attatgaccc catgattgcg 300
```

```
aagtgggtcg tgtgggcagc agatcgccag gcggcattga caaaactgag gtacagcctt 360
cgtcagtaca atattgttgg actgcccacc aacattgact tcttactcaa cctgtctggc 420
caccagagt ttgaagctgg gaacgtgcac actgatttca tccctcaaca ccacaaacag 480
ttgttgctca gtcggaaggc tgcagccaaa gagtctttat gccaggcagc cctgggtctc 540
atcctcaagg agaaagccat gaccgacact ttcactcttc aggcacatga tcaattctct 600
ccattttcgt ctagcagtgg aagaagactg aatatctcgt ataccagaaa catgactctt 660
aaagatggta aaaacaatgt agccatagct gtaacgtata accatgatgg gtcttatagc 720
atgcagattg aagataaaac ttccaagtc cttggtaatc tttacagcga gggagactgc 780
acttacctga aatgttctgt taatggagtt gctagtaaag cgaagtgatt atcctgaaa 840
acactattta cctattttcc aaggaaggaa gtattgagat tgacattcca gtcccaaat 900
acttatcttc tgtgagctca caagaaactc agggcgggccc cttagctcct atgactggaa 960
ccattgaaaa ggtgtttgtc aaagctggag acaaagtga agcgggagat tccctcatgg 1020
ttatgatcgc catgaagatg gagcatacca taaagtctcc aaaggatggc acagtaaaga 1080
aagtgttcta cagagaaggc gctcaggcca acagacacac tcctttagtc gagtttgagg 1140
aggaagaatc agacaaaagg gaatcggaat aaactccagc aaggaaatgg ccagttaagt 1200
agtgtcttct ctctccacca aaaagaggaa gtgcctccag cttttctggg ggtctcataa 1260
agagcagttt tactaaatga ttgtatgctt atgctgaaca cctttcatat tggagaatca 1320
tgcatttggg tctaataat tctcaaaata tttcatacta ataaagttga attatttttt 1380
attggaagcc aaaa                                     1394
```

00673395.122700

## (2) INFORMATION ON SEQ ID NO. 31:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 734 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

gccgacaaga tgttcttgct gcctcttccg gctgcggggc gagtagtcgt cgcacgtctg 60
gccgtgagac gtttcgggag ccggagtctc tccacgcag acatgacgaa gggccttggtt120
ttaggaatct attccaaaga aaaagaagat gatgtgccac agttcacaag tgcaggagag180
aattttgata aattgttagc tggaaagctg agagagactt tgaacatata tggaccacct240
ctgaaggcag ggaagactcg aaccttttat ggtctgcata aggacttccc cagcgtggtg300
ctagttagcc tcggcaaaaa ggcagctgga atcgacgaac aggaaaactg gcatgaaggc360
aaagaaaaca tcagagctgc tgttgacgag ggtgacagg agattcaaga cctggagctc420
tcgtctgtgg aggtggatcc ctgtggagac gctcaggctg ctgcggaggg agcgggtgctt480
ggtctctatg aatacgatga cctaaagcaa aaaaagaaga tggctgtgtc ggcaaagctc540
tatggaagtg gggatcagga ggcctggcag aaaggagtcc tgtttgcttc tgggcaagaa600
cttgggcacg ccaatttgat gggagacgcc agccaattga gattgacgcc aaccagattt660
tgccgaaatt atttgagaag attttcaaaa ttggtagtta gttaaaaccg aggtcctttt720
cagaccccaa tttt

```

734

## (2) INFORMATION ON SEQ ID NO. 32:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 692 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

004221" 55E4960

tgcagcgcgt	gcgtgctgcg	ctactgagca	ggcgcattgga	ggactctgaa	gcactgggct	60
tgcgaacacat	gggcctcgat	ccccggctcc	ttcaggctgt	caccgatctg	ggctggtcgc	120
gacctacgct	gatccaggag	aaggccatcc	cactggccct	agaagggaag	gacctcctgg	180
ctcggggccc	cacgggctcc	gggaagacgg	ccgcttatgc	tattccgatg	ctgcagctgt	240
tgctccatag	gaaggcgaca	ggtcgggtgg	tagaacaggc	agtgagaggc	cttggtcttg	300
ttcctaccaa	ggagctggca	cggcaagcac	agtccatgat	tcagcagctg	gctacctact	360
gtgctcggga	tgtccgagtg	gccaatgtct	cagctgctga	agactcagtc	tctcagagag	420
ctgtgctgat	ggagaagcca	gatgtggtag	tagggaccct	atctcgcata	ttaagccact	480
tgcagcaaga	cagcctgaaa	cttcgtgact	ccctggagct	tttggtgtgt	gacgaagctg	540
acctctcttt	ttcccttttg	ctttgaagaa	gagctcaaga	agtcttcctc	tggtcacttt	600
gcccccggt	tttaacaag	cttttctcat	gtcagctact	tttaacgagg	acgtacaagc	660
actcaaggag	ctgatattac	ataagccggt	at			692

```
ctgccacgca cgactgaaca cagacagcag cgcctcgcc atgaagctgc tgatggctct 60
catgctggcg gccctcctcc tgcactgcta tgcagattct ggctgcaaac tcctggagga120
catggttgaa aagaccatca attccgacat atctatacct gaatacaaaag agcttcttca180
agagttcata gacagtgatg ccgctgcaga ggctatgggg aaattcaagc agtgtttctc240
caaccagtca catagaactc tgaaaaaactt tggactgatg atgcatacag tgtacgacag300
catttggtgt aatatgaaga gtaatttaact ttacccaagg cgtttggtct agaggggtac360
agactatggc cagaactcat ctgttgattg ctagaacca cttttctttc ttgtgtgtgc420
tttttatgtg gaaactgtat gacaactgtt gaaacctcaa attcatttcc atttcaataa480
actaactqca aatcacaaaa aaaaaaaaaa gtcgacg 517
```

## (2) INFORMATION ON SEQ ID NO. 34:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 322 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
tcaagctgtg ggtgagaagc tctctagcag ggactctgac cttatggagg atcgctgttt 60
ccccatttt tccttttcac ccaaaaaagt cctgcttctg tcacccttca aacagcctgt120
gagcctaaat ttttgtggcc atgggacaga caaggacccc gtcttcagct gaactaaggal80
aaagtctctgc gacatctttg gccatcaaac tccaacccag tcacccaacc agagcctctg240
aggaatggcc ccttcttgcg gggaaccctt tacaatgggc ctcttgactg atgtttcccc300
aaaacagtgc ccctgtcatc ag                                     322
```

## (2) INFORMATION ON SEQ ID NO. 35:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1559 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

002221 5552950



(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```
gcacgagttg agagtgagtg tgtgtgtgtg cgtgtgcacg tgcacacatg tgcacggttg 60
tatgtatggg aaataaaactt ataaatgggg acgtattgga gaaggaaata catagacctt 120
caactttgag caaatagcag tgatgtttta ggaactgaaa tgcacactt aaagtcttca 180
gcccagctac ttccctatth ttggcgggga gaagagggcc tgattagaac tgttctgggt 240
gtgtttggcg ggaggggaat aatttttgtt cagtccttct tagtgaccaa actttaattt 300
ttaagaataa tatattgact tactgaactg aagcattctg agttgaaagg agctccagag 360
gagtggagtt ctgtgttgct cacatgttaa aagcttgctc accttcagag cagagggaat 420
acctatcttc agatatccgc ccattttcat ctcttcatta tagtcaaaca gtgtgacttg 480
agagtgttgc tctgggtgtc gtattctggc ttatgaagat tatttgaaaa agaactctta 540
ctacattgaa atgcagactt ttaaaaaatt aaatattgga ttaggcagtc aaaaaacca 600
acaagcataa aaggtcaata agttgtaata ttaaaagtaa aggtggaaaa ctctattata 660
atggaagaaa agttttgatt tccttttttg tttgatgggc agtatgcat attataccca 720
aagttctttt aaaaaatatt tccatcaacc atttttattt aaaataaaca tttgagggaa 780
gttaccaagg cagctttttt cctcaaaagt aacctgttcc tctttggaat agcacatttt 840
aggggcatgg ttaataacct agatttttac tcagtaaata ctgatgggta ctgtgtgtaa 900
aatatcttta agtaggattg aaggcctctg tgggggaata aaatattacc aaagtctata 960
aaaataaatt ttacatgttc tcttttatga cagagagcag cactgggtct gttattttta 1020
aaatgaataa ttgatttctt gatagggtgt taatatttct tccctcactg ctgattctta 1080
gatagaaacc attctttata tttgatagac tgctttcaga aaaccttat caacaagtgt 1140
acaatactta tctaaaacta tacatttaga atggagcagt ttaatactag atctcagaag 1200
ttttgaaaaa tagcaaaaga gactggattt ggaaagcatg gtctacaatt ggttggttaa 1260
ttctgaagct atgaagaata aatgtttcaa ctttgatta tgaaacocca tttatgattt 1320
tttaaataca cttgaaataa aaatgattaa actaaatttt ggtccagtga cattactttg 1380
cactgcataa tccattatac gttgtacgac tttttttttt ggtttgaatt aataactgag 1440
agttttgtgt gaagctacgg catatctaac cggagaattt cggatgcctt atacggtgat 1500
tatattatat gggggcattt gtagtgcagc ggaagacgga atttatgcct ttgggaaac 1559
```

(2) INFORMATION ON SEQ ID NO. 36:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

004227 563395 122700

## (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

cacacgtgct gacggcgggg acattcacat ccataagaag aaatctcagc aagtgttcgc 60
gtccccagct aaacaccccca tggacagcaa gggggaggag tocaagatca gctaccccaa 120
catcttcttc atgattgaca gcttcgagga ggtgttcagc gacatgaccg tagggaagga 180
gagatggctct gtgtggagct ggtggctagt gacaaaacca acacgttcca gggggtcac 240
tttcagggct ccatccgcta cgaggcgctc aagaagggtgt atgacaaccg ggtgagcgtg 300
gccgcccgc tggcacagaa gatgtcgctt ggcttctaca agtacagcaa catggagttt 360
gtgcgcatga agggcccccga gggcaagggc cagcgcgaga tggcggtcag ccgagtgtct 420
acaggtgaca cagccccctg tgggactgaa gaggactcca gccagcttc gcccatgcac 480
gagcgggtga cctccttcag cagaccccc accccagaac ggaacaaccg gcctgccttc 540
ttctcccat cctcaagag gaagggtgcc cggaaccgga tcgctgagat gaagaagtcg 600
cactcgccca acgacagcga ggagttcttc cgggaggacg acggtggagc cgatctgcac 660
aatgcaacca acctgcggtc tcggtccctg tcgggcacag gacggtccct ggtcgggtcc 720
tggctgaagc tgaacagagc agatggaaac ttcttctct atgcacactt aacctacgtc 780
acgttgccgc tgcctcgat ttaacagac atcctggaag ttggcgagaa gcccatcctg 840
atgacctagc cgcgtgcgga gcctgcgcag agccccggcc gggcccagcc ctcgaggtgc 900
tgccaagtgc ctacctgtcc accgccaccg gggctctgca tggcacgcca gtgttggagc 960
cgcagccagg cgaggccact cgactgccgg ggccggggcc gactgcacga acaccagccc 1020
aaactgaagt gcctctgacg ggccctgctg gcgctgcttc cgccctgtgc cc 1072

```

## (2) INFORMATION ON SEQ ID NO. 37:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 454 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

gtgctgcatg gagtgagtgg cggcatccac cgtgaggagg agaggagctc tgataccctc 60
aggacccgcc aggaggggca tcacggaggc ttctggacga cttggagctg tgctctgggg 120
agaaaaccgc tcctgtgtgg gccctgagtg ctgaggagga agctgccatg cacttttccc 180
tggcattttt cctgcatggt tcgtctgttt ttttgcaaat aacatgttgt catgaatttt 240
tatgcatgag gcatatttca tcatgtctgt atgctgaagt ccccttcac ctttcaattg 300
gttggtggac aggagagaga ggtccaaggt gccctacac gtgcccagc gccgtgggag 360
gagatcgagc gccgaggcac ggaggaggtg ggcctctacc gcatgtctgg ggtggccgca 420
gacatccagg cactgaaggc agccttcaac gtca 454

```

002227"56EE2960

## (2) INFORMATION ON SEQ ID NO. 38:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 700 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

cttgctcgag ccctaaccag gggatatctt gagcctgggt ggatccccgg agcgtcacat 60
cactttccga tcacttcaaa gtgggttaaaa actaatattt atatgacaga agaaaaagat120
gtcattccgt aaagtaaaca tcatcatctt ggtcctgggt gttgctctct tcttactgg180
tttgaccat aacttctctc gcttgagcag tttgttaagg aatgagggtta cagattcagg240
aattgtaggg cctcaacctc tagactttgt cccaaatgct ctccgacatg cagtagatgg300
gagacaagag gagattcctg tggtcacgc tgcacatgaa gacaggcttg gggggggccat360
tgcagctata aacagcattc agcacaacac tcgctccaat gtgattttct acattgttac420
tctcaacaat acagcagacc atctccgggt ctgggtcaac agtgattccc tgaaaagcat480
cagatacaaa attgtcaatt ttgaccctaa acttttggaa ggaaaagtaa aggaggatcc540
tgaccagggg gaatccatga aacctttaac ctttgcaagg ttctacttgc caattctggg600
ttcccagcgg caaaggaagg cccgtttaca tgggggtgat gatgttattt gtggcagggtg660
ggattttttg ccctttacat tacagcagtg aggccggggc 700

```

## (2) INFORMATION ON SEQ ID NO. 39:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 914 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

0022275652960

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```
ccggcctgcg gtgggcagca gctcagggtc tccaaatcat tgcgtagtgc cgaataccct 60
cggccacacc tggccttctc catgctcggg ataacttcct gcagcgacca acaggctaaa120
gagggggaag ggatccagca ccggctcctc ctccggcaac cacggtggga gcggcgagg180
aaatggacat aaacccgggt gtgaaaagcc agggaatgaa gcccgcggga gcgggaaatc240
tgggattcag ggcttcagag gacaggaggt ttccagcaac atgagggaaa taagcaaaga300
gggcaatcgc ctccctggag gctctggaga caattatcgg gggcaagggt cgagctgggg360
cagtggagga ggtgacgctg ttggtggagt caatactgtg aactctgaga cgtctcctgg420
gatgtttaac tttgacactt tctggaagaa ttttaaatec aagctgggtt tcatcaactg480
ggatgccata aacaagaacc aggtcccggc cccagcacc cgagccctcc tctacttcag540
ccgactctgg gaggatttca aacagaacac tcctttcctc aactggaaag caattattga600
gggtgcggac gcgtcatcac tgcagaaacg tgcaggcaga gccgagtcag aactacaatt660
acaaccagca tgcgtatccc actgcctatg gtgggaagta ctcagtcaag acccctgcaa720
agggggggag tctcaccttc ttccctcggt tcccgggtgc aacctgggcc tgcttgagct780
tgggtgaagt tttggtaagg caatttcttg caaccaacca ccgaaggccc cggaaaaagc840
actgggttcg tcaagggaag ctccctcccc ctttggggcc ccagccttg tggcaggccc900
ctggggcccg gttg
```

914

(2) INFORMATION ON SEQ ID NO. 40:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1669 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

09673395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

gagctgcagc agagcaggta acagctcttg cacctgtttc tcttgcacct gacgtgcagc 60
tgctcctacc cacctctcct ggctgagcct tgcttgatac agcagcccgg aggcaccact 120
tgcttcccga gtctcaccct cccaggcagc tcctacactc aactgcttct ctaggaaagg 180
tctcaccctcc agcctggagc agtcgggatt acagaaagcc ccacctcttg cttaggaggc 240
gccatgacga ctgaaatttg ttggtggaag ctgactttcc tccggaaaaa gaaatccact 300
cccaaagtgc tgtatgagat ccctgacacc tatgccccaa cagagggaga tgcagaaccc 360
ccgaggcctg acgctggagg ccccaacagc gactttaaca cccgcctgga gaagattgtg 420
gacaagagca caaagggcaa gcacgtcaag gtctccaact caggacgctt caaggagaag 480
aagaaagtga gagccacgct ggcagagaac cctaacctct ttgatgatca cgaggaaagg 540
cggatcatca agtgaagggc tgaggagggt gctagcacct cttggctccc tgccatcagc 600
cagatctgag acaggacctt gccacgctgg cctctttggc catagctgaa gctgtggggc 660
cagttgatag ctgctggcag gaaatggctg ttttttaggt ttgtatttat gtgccgccac 720
ttttgtaagg cctgggagat cccagggtcc tccaccctcc ccctgaccac atacaaaggc 780
actctagttc aagagtgaag agtctcaccg aggaggaaca gccctccttg aagcaatggc 840
agggccagca gggagggtgg catggcaggg aatggagaga gtgagccaga cagacttcac 900
ctccttactg gacacagggt caaggcgag ttccaattgc tgctcccttt actttctcta 960
cctgtgacta ctccctggac caatcctgag gagggcacat tttccagaag ccacgtgata 1020
ggggctggtt tctgtggagc cagaggcaga gacactgaac ttgagctcac ctccaaacac 1080
cggcagtaaa ctccctggaa ctttgccctc aggtgcggag gggacagagg accctggcac 1140
tctgttaggg tgctgtagaa gactagattg atggtagttt ggctgttag ttctgttttt 1200
ggccatgact tttgcagatg gcaagtcaca caccctcaaa gggaagctac acgggccaaa 1260
tcgggggagt ggggtgggaa ttttctcctc tccctttcct actataatag tatttaagac 1320
atatcagctc cagagatgag tctggagacc ttgaattttg ttttaacaaa taattgtagg 1380
tttctctctg taataacaac gctggaaagg cagagaacct cttttatgct catgtcttgc 1440
atttattgag atgactgttt ctcatgcctt tatgttcctt catgtaagta aagtggacct 1500
ttgtgctcaa aaaaaaatt tcaagcttca ggaagggtt cccaagggtg gacaatgtag 1560
gaacctgggt cactaatatt taccatcaaa cctagcetta gtatgggat ggggcaagca 1620
gaaggagcta gttacacctc agtggtcagt tctctccagt caacagaga 1669

```

## (2) INFORMATION ON SEQ ID NO. 41:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 355 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002221 5652960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

ccggcctccc ctcgctctga ggctcggggg cccagctcc gcgtaaactg cacgatttcg 60
ccctctgctc agctccccctc tgccccctct ttccaagaga gacttccaga tcccacattt120
tcttgactga ttttgaagct gtctgtttgc attctgattg ggaacactgg gatcattttc180
atcatgccga cagtgggtgt aatggatgta tccctttcca tgaccgacc tgtgtctatt240
gaggggtccg aggaatacca gcgtaagacc tagcagcca tggtttaacg atgcttggtt300
tgagcacatg gccacaaatt acaagcttga atttacagca cttgtgggtt ttca      355

```

## (2) INFORMATION ON SEQ ID NO. 42:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2628 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227-5622960

gqgtgqgcct	gctttcgccc	tctttctcca	gcgggagggg	cgcggaacttc	cgcgggggcgg	60
agtcctgtcta	gtgctgacgt	tggcagccga	acccaaagta	gatcgaggcg	gcgggctgca	120
cattcccgtt	gttgcgttgc	gtttccttec	tctttcactc	cgcgctcacg	gcggcggccca	180
aagcggcggc	gacggcgggc	cgagaacgac	ccggcggccca	gttctcttcc	tcttgcgcac	240
ctgcctgtct	cggtcagtcg	gtcggcgggc	ggcgcccggc	ttgtgctcag	acctgcgcgt	300
tgcggcgccc	aggcccagcg	gccgtagcta	gcgcttgccc	tgagaacctc	ggcgctccgg	360
cggcgcgggc	accacgagcc	gagcctcgca	cgcgctccag	aggagcgagg	cgagtgagcg	420
agtcgagggg	gtggccgggg	cagggtggtg	gcgcgcgaag	atggtcgcca	agcaaaggat	480
ccgtatggcc	aacgagaagc	acagcaagaa	catcacccag	cgcggaacg	tcgccaagac	540
ctcgagaaat	gccccgaag	agaaggcgct	tgtaggacct	tggttattgg	ctctcttcat	600
ttttgttgtc	tgtggttctg	caattttcca	gattattcaa	agtatcagga	tgggcatgtg	660
aagtgactga	ccttaagatg	tttccattct	cctgtgaatt	ttaaactgaa	ctcattcctg	720
atgtttgata	ccctggttga	aaacaattca	gtaaagcatc	ctgcctcaga	atgactttcc	780
tatcatgctt	catgtgtcat	tccaaggttt	cttcatgagt	cattccaagt	tttctagtcc	840
ataccacagt	gccttgcaaa	aaacaccaca	tgaataaagc	aataaaaattt	gattgttaaag	900
atacagtagt	ggaccctaet	tattcagtcg	attaagagta	agtttttttta	tgtgggttatt	960
aaaacagtat	gaacaattag	tctaactctg	catagacagg	gtctagattt	tgttaaccca	1020
aatgtataac	tgcagtttag	ttaaattaca	atttgaagtc	ttgtggtttt	tatatagcta	1080
ggcactttat	tactcttttg	aactgaaagc	acactccctc	ataggttcat	gtaactgtcc	1140
tgttaataag	tgcttataaa	tggaaaacct	acacggccta	gtttttgccac	aaccttttagc	1200
atctaaaaag	ttttaaaagc	ttctaaatgt	ctaataataa	gggagatgct	tatagccaca	1260
acatctattt	taccaatatt	gtttccatta	cactaccttg	gattttgcat	gagtgagtat	1320
agtaacccaa	gatgccataa	aaaaaaactt	gatcgttttc	tgacttaatc	agttactgtg	1380
gtttcactaa	aagctaccgt	ggtggagtga	agtcagtcag	ggaaggtttg	tttatgttacl	1440
atttattttca	ccagaactat	tttaatatat	caaagggggt	tactatgcca	aacaaaattcl	1500
tcaggaaaaa	tactgtctaa	aatggatgcc	tcattcagaac	atgctgttga	gtccaatgtg	1560
ccataagaca	ttttagcatg	ttaaatagca	cttttaaatg	caaaaaaagg	cacatcaact	1620
cggaagtgtat	ccttagtttg	caaatgcctt	ttctagatta	atgatttttc	aatcattaggl	1680
gtactagaca	catcagccta	aagtggcatc	tggaaattgaa	tggatttact	gataatgatc	1740
agtcttttagt	cttccctttg	ttatatgact	ttataggtta	tgattgatca	aatttacggt	1800
ttactaatgg	taagggtgag	ggtcataggg	caggtttttg	gttttctagt	actggtgaaa	1860
actgcaagta	ttggctattt	gtatacttag	ccataacttg	gtgaaaaaaa	acctgagcag	1920
tgtctatgta	ttaatgcgtt	ggaaagaaa	ctgcttgtgt	ttgcttttgt	aatgtcctca	1980
ggatattttc	tttaaaaata	gctgttttaa	gaggaaacga	agggaaactc	gtcacttagt	2040
ctatacacag	cgtgaacctc	acagggggct	tctgatcccc	tcaaacatgg	agaacagtaa	2100
gggagcgag	tggttaaagga	ctttcaggaa	cttaactatt	ctggaataag	gaatgaatca	2160
actgaccttg	ggccagcagg	tttttaacta	aattgttact	tgcttttctc	accagttaaa	2220
tcagtctctg	tacttgtttc	cctttttgaa	acaagtgctc	tggttaacta	attctgtttt	2280
atggttggtc	taaattcata	gcaggtgctc	tattctttgc	ttttagtcaa	accattccat	2340
atcagaattt	tccttggttt	actatagata	tttggcttta	agttgttgtt	tgtgtttttt	2400
aatgtacaat	gttctgatac	atttgactgt	taaattgcta	tagctatgaa	tcattttaca	2460
tattgaaaaa	tgcattccct	ttgtatttca	tgtgtaattc	accaattaa	tgagttttat	2520
attcagggtg	gattatgcat	gtttaggtaa	acgaaagctg	tgtcttactt	gatttattct	2580
ttaaaaataa	agttccctga	atatttgaaa	aaaaaaaaaa	aaaaaaaaaa		2628

## (2) INFORMATION ON SEQ ID NO. 43:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2535 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227-56E2960



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

agttcggcac agggggagga acctggccct gggaggagggc tgttgctgtgc tcctacagaa 60
tcccgttctg aagggaagag catgtttgcg ggcgtcccca ccatgcgtqa qaactcccc 120
aaacagtaca tgcagctcgg aggcagggtc ttgctggttc tgatgttcat gaccctcctt 180
cactttgacg ccagcttctt ttctattgtc cagaacatcg tgggcacagc tctgatgatt 240
ttagtggcca ttggttttaa aaccaagctg gctgctttga ctcttggtgt gtggctcttt 300
gccatcaacg tatatttcaa cgccttctgg accattccag tctacaagcc catgcatgac 360
ttcctgaaat acgacttctt ccagaccatg tcggtgattg ggggcttgct cctgggtggtg 420
gcccctgggc ctgggggtgt ctccatggat gagaagaaga aggagtggta acagtcacag 480
atccctacct gcctggctaa gaccctgggc cgtcaaggac tgggttcgggg tggattcaac 540
aaaactgcca gcttttatgt atcctcttcc ctccccctcc cttggtaaaag gcacagatgt 600
tttgagaact ttatttgcag agacacctga gaatcgatgg ctgagtcctgc tctggagcca 660
cagtctggcg totgacctt cagtgcaggc cagcctggca gctggaagcc tccccacgc 720
cgaggctttg gagtgaacag cccgcttggc tgtggcatct cagtcctatt tttgagtttt 780
tttgtggggg tacaggaggg ggccttcaag ctgtactgtg agcagacgca ttggtattat 840
cattcaaagc agtctccctc ttatttghta gtttacattt ttagcggaaa ctactaaaatt 900
attttgggtg gttcagccaa acctcaaaac agttaatctc cctgggttaa aatcacacca 960
gtggccttga tgttgtttct gccccgcatt gtattttata ggaatagtga aaacatttag1020
ggacacccaa agaattgatgc agtattaaag ggggtggtaga agctgctgtt tatgataaaa1080
gtcatcggtc agaaaatcag cttggattgg tgccaagtgt tttattgggt aacaccctgg1140
gagtttttagt agcttgaggc aaggtggagg ggcaagaagt ccttgggggaa gctgctggtc1200
tgggtgctgc tggcctccaa gctggcagtg ggaagggcta gtgagaccac acaggggtag1260
ccccagcagc agcacccctgc aagccagcct ggccagctgc tcagaccagc ttgcagagcc1320
gcagccgctg tgggcagggg gtgtggcagg agctcccagc actggagacc cacggactca1380
acccagttac ctcacatggg gccttttctg agcaaggtct cgaaaagcga ggccgacctg1440
gctgagcagc accgcccctt cccagctgga ctgcgccctg ggacagcccc gacacaccac1500
tttcttgagg ctgtcgtca ctacagattgt ccgtttgcta tgccgaatgc agccaaaatt1560
cctttttaca atttgtgatg ccttaccgat ttgatcttaa tcctgtattt aaagttttct1620
aacactgcct tatactgtgt ttctcttttt gggggagctt aactgcttgt tgctccctgt1680
cgtctgcacc atagtaaagt ccacaagggt agtcgaacac ctctctggcc cctagacctal1740
tctggggaca ggctggctca gcctgtctcc agggctgctg cggccagacc ccgagcctgc1800
ctccctcttg gcctctcatc cattggctct gcagggcagg ggtgaggcag gtttctgctc1860
ataagtgctt ttggaagtca cctacctttt taacacagcc gaactagtcc caacgcgttt1920
gcaaatatcc cctggtagc ctacttccct acccccgaat attggttaaga tcgagcaatg1980
gcttcaggac atgggttctc ttctcctgtg atcattcaag tgctcactgc atgaagactg2040
gcttgtctca gtgtttcaac ctccaccagg ctgtctcttg gtccacacct cgctccctgt2100
tagtgccgta tgacagcccc catcaaatga ccttggccaa gtcacggttt ctctgtggtc2160
aaggttgggt ggctgattgg tggaaagtag ggtggaccaa aggaggccac gtgagcagtc2220
agcaccagtt ctgcaccagc agcgccctcg tcctagtggg tgttcctgtt tctcctggcc2280
ctgggtgggc tagggcctga ttcggaaga tgcctttgca gggaggggag gataagtggg2340
atctaccaat tgattctggc aaaacaattt ctaagatttt tttgctttat gtgggaaaca2400
gatctaaatc tcattttatg ctgtatttta tatcttagtt gtgtttgaaa acgtttttgat2460
ttttggaaac acatcaaaat aaataatggc gtttgttgta aaaaaaaaaa aaaaaaaaaa2520
aaaaaaaaaa aaaaaa
2535

```

0967396-122700

## (2) INFORMATION ON SEQ ID NO. 44:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 805 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

ggcaccgagcg gcaccgagcca tctccatccc cggagcatct gtatgattca gaagtacaac 60
cacgatgggg aagcagggtcg gctggaggct tttagccaag gggaaagtgt cctaaaggaa120
cccaagtacc aggaagagct ggaggacagg ctgcatttct acgtggagga atgtgactac180
ttgcaggggt tccagatcct gtgtgacctg cacgatggct tctctggggg aggcgcgaag240
gcggcagagc tgctacaaga tgaatattca gggcggggaa taataacctg gggcctgcta300
cctgggtccct accatcgtgg ggaggccag agaaacatct atcgtctatt aaacacagct360
tttgggtctcg tgcacctgac tgctcacagc tctcttgtct gcccttgctc cttgggtggg420
agcctggggc tgcgacccga gccacctgtc agcttccctt acctgcatta tgatgccact480
ctgcccttcc actgcagtgc catcctgggt acagccctgg acacagtcac tgttccttat540
cgctctgtgt cctctccagt ttccatgggt catctggctg acatgctgag cttctgtggg600
aaaaagggtg tgacagcagg agcaatcacc cctttccctt tggctccagg ccagtcctt660
cctgattccc tgatgcagtt tggaggagcc accccatgga cccactgtg tgcatgtgg720
gagccttctg gaacacgttg ctttgcccag tcagtgggtg tgagggggta tagacagagc780
atgccacaca agccacagac ttaat

```

805

## (2) INFORMATION ON SEQ ID NO. 45:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

002227 55552960

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

cggaagtagc cgcaggcatg gcggcggtta tgccgctgtt gctctgctcg tcctgttgct 60
cctggggccc ggccggctggt gccttgacaga acccccacgc gacagcctgc gggaggaact 120
tgtcatcacc ccgctgcctt ccggggacgt agccgccaca ttccagttcc gcacgcgctg 180
ggattcggag cttcagcggg aaggagtgtc ccattacagg ctctttccca aagccctggg 240
gcagctgacg tccaagtatt ctctacggga gctgcacctg tcattcacac aaggcctttg 300
gaggaccgga tactgggggc cacccttcct gcaggcccca tcaggtgcag agctgtgggt 360
ctggttccaa gacactgtca ctgatgtgga taaatcttgg aaggagctca gtaatgtcct 420
ctcagggate ttctgcgcct ctctcaactt catcgactcc accaacacag tcaactccac 480
tgccctcctt aaacccttgg gtctggccaa tgacactgac cactacttct tgcgctatgc 540

tgtgtgcccg cgggaggtgg tctgcaccga aaacctcacc ccctggaaga agctcttgcc 600
ctgtagttcc aaggcaggcc tctctgtgct gctgaaggca gatcgcttgt tccacaccag 660
ctaccactcc caggcagtgc atatccgccc tgtttgacaga aatgcacgct gtactagcat 720
ctcctgggag ctgaggcaga ccctgtcagt tgtatttgat gccttcacat cggggcaggg 780
aaagaaagac tggtcctctt tccggatgtt ctcccgaacc ctacaggagc cctgccccct 840
ggcttcagag agccgagtct atgtggacat caccacctac aaccaggaca acgagacatt 900
agaggtgcac ccacccccga cactacata tcaggacgtc atcctaggca ctcggaagac 960
ctatgccatc tatgacttgc ttgacaccgc catgatcaac aactctcgaa acctcaacat 1020
ccagctcaag tggaagagac cccagagaaa tgaggccccc ccagtgccct tcctgcatgc 1080
ccagcggtag gtgagtggct atgggctgca gaagggggag ctgagcacac tgctgtaca 1140
caccaccca taccgggctt tcccgggtgt gctgctggac accgtaccct ggtatctgcg 1200
gctgttacat ccactaccag cctgcccagg accggctgca accccacctc ctggagatgc 1260
tgattcagct gccggccaa
1279

```

(2) INFORMATION ON SEQ ID NO, 46:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1923 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

09673395 122700

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

gcgcaagaca caggaggccc aggcggcag tcaggacatg gcggcgattt gcagattcca 60  
atctctctgt ttctgcggcg attgaacacc caacattggc gaccgggatc gcggaaagtg 120  
atggctgtcg tcccggcgctc tctctcagga caggacgtgg gatcatttgc atatcttaca 180  
attaaagaca gaataccaca gatcttaact aaggttattg atacattgca tcgacataaa 240  
agtgaatttt ttgagaaaca cggagaggaa ggcgtggaag ctgaaaagaa agctatctct 300  
ctcctttcta aattacggaa tgaattgcaa acagataaac catttatccc cttggttgag 360  
aaattttgtg atactgatat atggaatcag tacctagaat atcaacagag tctttttaa 420  
gaaagtgatg gaaaatcaag atggttctac tcaccgtggt tgttggtaga atgttacatg 480  
tatcgaaaga ttcatagaagc aattatccag agtccaccaa tcgattactt tgatgtattt 540  
aaagaatcaa aagagcaaaa tttctatggg tcacaggaat ccatcattgc tttatgtact 600  
cacctgcaac aattgataag aactattgaa gacctagatg aaaatcagct gaaagatgag 660  
tttttttaaac ttctgcagat ttcactgtgg ggaaataagt gtgatctgtc tctctcaggt 720  
ggagaaagta gttctcagaa taccaatgta ctaaattcat tggagacct aaaacctttc 780  
attttattga atgatatgga acatctttgg tcattgctta gcaattgcaa gaaaacaaga 840  
gaaaaagctt ctgctactag agtgatatatt gttctcgata attctggatt tgagcttgtt 900  
acagatttaa tattagccga cttcttggtt tcctctgaac tggctactga ggttcatttt 960  
tatggaaaaa caattccatg gtttgtttct gatactacta tacatgattt taattggtta 1020  
attgaacagg taaaacacag taatcataag tggatgtcca agtgtggggc tgactgggaal 1080  
gagtatatta aaatgggtaa atgggtttac cacaatcata tattttggac tctgcctcat 1140

gagtactgtg caatgcctca ggttgacact gacttatatg ctgaactaca gaaggcacat 1200  
ttaattttat tcaagggtga tttgaattac aggaagtga caggtgacag aaaatgggag 1260  
ttttctgttc catttcatca ggctctgaat ggcttccatc ctgcaccact ctgtaccata 1320  
agaacattaa aagctgaaat tcaggttggt ctgcagcctg ggcaagggga acagctcctg 1380  
gcctctgagc ccagctggtg gaccttgga aaatatggaa tatttcagta cgatggtccc 1440  
ctttgacttg atttaggagc tctcagttgc atagaaagat ctggtgagca ctttttcatt 1500  
cccagaaaag gagcacgtga attgagtcgc ctggcggctc tgtacgcgct cagggaagct 1560  
tagcttcttg gtgcccattc acgtgcactg gatgattttt cttttgaaca ttttgcccc 1620  
ctacactgtt tttggggata gctgggttaa gcaagttaaa gatatttaca tttatattgg 1680  
agatttttaag caactttttt ttcagggtaa atatataatt tcaaagtgtc tttaaatgg 1740  
ccttaatttt gaagtgggta gggccaaaaa ataaaggag ggctcctttg aggtaggtac 1800  
ccttggcctt tcctaaaaag cccctcaatg ggatttagat ccgggggggt ggggttattt 1860  
tccttggttt ggccatgaaa atccttgga cggccttatg cccttttgaa aaggggggtt 1920  
ttt 1923

0967339E 122700

## (2) INFORMATION ON SEQ ID NO. 47:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 706 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

cattttacga caggcgggat tgttttgtgg ctgtcagctt tctccgtggt ctgagtttgt 60
ggctgcattt ttatctctgg tggctctgct acggcggcgc agaaatgagg cagaagcggal20
aaggagatct cagccctgct gagctgatga tgctgactat aggagatggt attaaacaac180
tgattgaagc ccacgagcag gggaaagaca tcgatctaaa taagggtgaaa accaagacag240
ctgccaaata tggcctttct gccagcccc gcctgggtgga tatcattgct gccgtccctc300
ctcagtatcg caaggtcttg atgcccaagt taaaggcgaa acccatcaga actgctagt360
ggattgctgt cgtggctgtg atgtgcaaac cccacagatg tccacacatc agttttacag420
gaaatatatg tgtatactgc cctgggtggac ctgattctga ttttgagtat tccaccag480
cttacactgg ctatgagcaa cctccatgag agctattccg tgccagatat ggaccctttt540
ccttacagga caaggacacc ggattaggaa cagtttaaaa caagttgggt tcgtagtg600
gggttaagtg ggagtttgtt tgtggatggg gtgggaactt tttggggccg ttccagagga660
ttacagagtt atttttattt cggaaagtta cgtgatgggt tttccg 706

```

## (2) INFORMATION ON SEQ ID NO. 48:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 749 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

002221 5652960

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

gacctatcct catctgtgca aggaggagt gccaaactct gagcccaggc tgttgcttcc 60
tggtctgggt gtgaatcctc catagtctgg tgagtgtagt gcccaactct ggagcccagg120
atgttgcttc cgggtctggt ggtgaatcct ccatagtctg gagatctcag ccctgctgag180
ctgatgatgc tgactatagg agatgttatt aaacaactga ttgaagccca cgagcagggg240
aaagacatcg atctaaataa ggtgaaaacc aagacagctg ccaaatatgg cctttctgcc300
cagccccgcc tgggtggatat cattgcttgc cgtccctcct cagtatcgca aggtcttgat360
gcccaagtta aaggcgaaac ccatcagaac tgctagtggg attgctgtcg tggctgtgat420
gtgcaaacc cagagatgtc cacacatcag ttttacagga aatatatgtg tatactgccc480
tgggtgggac ctgattctga ttttgagtat tccaccaggt cttacactgg gctatgagcc540
aacctccatg aggagctatt ccgtgccaga tatggaccct tttccttaca ggacaaggac600
accgatttag gaacagttta aaacaagttg gggtcgtagt gtgggggttaa gtgggagttt660
gtttgtggat ggggtgggaa ctttttgggg ccgttcagga ggattacaga gttattttta720
tttcggaagt ttacgtgatg ggttttccg                                     749

```

## (2) INFORMATION ON SEQ ID NO. 49:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 857 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

0967395-12200

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

accttaccaa ggggagaaaa aaaccctcca ctttggtca ctgtgggttt ggcactaaga 60
ggcacgatat ctgaaggagg tcattccagt tttaaaagta cggacagtgc tgttggaact120
gaccacaaaa atgtattgtt aaaaaaaaaat tgaaaaccag cagtgatttg ggtcccctg180
aaacctctgt gaatcggagg tgggccagg aggtgacagg acgcagcaga aatagtccca240
gaaaggagag acgggtcatg cagcgggctt gtgctttttt gtgtgtgttt gtgtgtttta300
caccatacat ctccaaatga agtatttatt aacaattgta gtgtaagcct gtgataaaat360
agcacaaagg ttcttttaaag aagttcactt ttaaggcatc agaaaagtta atgtggcaaa420
catttttaatt aaaacatcag aagtaaattt tatttttaaac tttaggcctc tgaatttttc480
cagtaaacac agttcagcta tgtggcaaag tcaatgggtg gcatctaaaa tgactttttta540
cattctacaa aaaaaataaaa taaaataagg acacagcccc aaacgggtgtc acctcttcgc600
ggcgcgtcca catgcacaga atctactagg atttgtcacg gccgggtggc acccgatttg660
ttttgactat acaacaaact tttttttcaa aagtatttgt tcaggataac tttaaaaata720
atataaaaat aaacaatgga tttgactttt ccctcaaaat tgaaaagaaa ggggtggggg780
gaggtgttaa ccattggcct tttttttttt ggaggggccc cattgggatt gtaaggccct840
ggggttccgg cctttcc
857

```

## (2) INFORMATION ON SEQ ID NO. 50:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 268 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

ccgcgcccgg cccccaggca attttaataa taaatcttaa tagatggggt aagagctgcc 60
ttcatcccat acagagaata caatggtgct agactaagta gagattttat ttcagcttaal20
agattctgtt tgatgtctga aattacatgt ttaggcggca tggggaacag gactgttctt180
tagcatcagt ttcacaatta cttaaatcta ctaggtttca ttcaccttat aattctgaaa240
tttcatcagc agtggggaac agaaaagg
268

```

002221 5652960

## (2) INFORMATION ON SEQ ID NO. 51:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 297 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

ctgatgtgca ctctagggtta gtaaccattt ttgtgaaaaa tttagagaaa ttctttgagc 60
agcttccact gaaacactaa aacccaatag ggccaaaggc ccataacctg aggaaacctt120
atattattgct taatccaaca taggctatga aagttttgag ttctctcttg tgtattagaal80
tttcattcct atttgttgta gagagtatag tacggggaat cagtaaatta aatgaagtaa240
actaaagatt acacctttgc tgctggcact aagcgaaaag caaaaccagt ggctgtc 297

```

## (2) INFORMATION ON SEQ ID NO. 52:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 590 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227 "56EE2960



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

acgggtcaaaa tgataactca tgtatTTTTat tccaacaaca tttggTTTTat aaaggaatac 60
aaacaggcac aaaacatggt tcagaagatt tattaagtaa acttgctaaa atatggacag120
atacacttag cagtcaaaca gttgaatatt cattgctacc tcattaaagt ttttgtatct180
gtattaccag gtccaaacat aaaaaccacc tctgttcaaa aaataaatgt tcagagagct240
gtatgttctt tgttctggta tgtacatttt aaaaaaacac ctctttccag tcttgctaac300
caagaatatt agtcatataa aagaacttag aatttttttc cccaagtaca agctatcttt360
tgctccaaaa cagttctgaa ggttttattt atattttatc ttatcccagag ggaccaacag420
caggcatacc tttgccaggc cttcttgtag aaagacacag agccgtaaag gcaaaaaataa480
aattgcaata aagtatatgg tattgggggc agggagaacc agaaaccctc aaggggacca540
atTTTTagca cgttctTTTT ttagggttta cctgtggag taagaactag 590

```

## (2) INFORMATION ON SEQ ID NO. 53:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227-5652960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

ggaaggggaa gtttcgcctc agaaggctgc ctcgctggtc cgaattcggg ggcgccacgt 60
ccgcccgtct ccgccttctg catcgcggtt tggcggtt ccacctagac acctaacagt 120
cgcgagccg gccgcgtcgt gagggggtcg gcacggggag tcgggcggtc ttgtgcatct 180
tggtacctg tgggtcgaag atgtcggaca tcggagactg gttcaggagc atcccggcga 240
tcacgcgcta ttggttcgcc gccaccgtcg ccgtgccctt ggtcggcaaa ctcggcctca 300
tcagcccggc ctacctcttc ctctggcccg aagccttcct ttatcgcttt cagatttgga 360
ggccaatcac tgccaccttt tatttccttg tgggtccagg aactggattt ctttatttgg 420
tcaatttata tttcttatat cagtattcta cgcgacttga aacaggagct tttgatggga 480
ggccagcaga ctattttatt atgctcctct ttaactggat ttgcatcggt attactggct 540
tagcaatgga tatgcagttg ctgatgattc ctctgatcat gtcagtactt tatgtctggg 600
cccagctgaa cagagacatg attgtatcat tttggtttgg aacacgattt aaggcctgct 660
atttaccctg gggtatcctt ggattcaact atatcatcgg aggctcggta atcaatgagc 720
ttattgaaa tctggttgga catctttatt ttttcctaag gttcagatac ccaatggact 780
tgaggaggaag aaattttcta tccacacctc agtttttcta ccgctggctg ccagtagga 840
gaggaggagt atcaggattt ggtgtgcccc ctgctagcat gaggcgagct gctgatcaga 900
atggcggagg cgggagacac aactggggcc agggctttcg acttgagac cagtgaaggg 960
gcggcctcgg gcagccgctc ctctcaagcc acatttcctc ccagtgtctg gtgcgcttaa 1020
caactgcgtt ctggctaaca ctgttggaac tgaccacac tgaatgtagt ctttcagtac 1080
gagacaaaag ttcttaaata ccgaagaaaa atataagtgt tccacaagtt tcacgattct 1140

cattcaagtc cttactgctg tgaagaacaa ataccaactg tgcaaattgc aaaactgact 1200
acattttttg gtgtcttctc ttctcccctt tccgtctgaa taatgggttt tagcgggtcc 1260
tagtgtgctg gcattgagct ggggctgggt caccaaacc ttcccaaaag gacccttctc 1320
tctttcttgc acacatgcct ctctcccact tttcccaacc cccacatttg caactagaag 1380
aggttgcca taaaattgct ctgcccttga caggttctgt tatttattga cttttgccaal 1440
ggcttggtca caacaatcat attcacgtaa ttttcccctt ttggtggcag aactgtagca 1500
atagggggag aagacaagca gcggatgaag cgttttctca gcttttgga ttgcttcgac 1560
ctgacatccg ttgtaaccgt ttgccacttc ttcagatatt tttataaaaa agtaccactg 1620
agtcagttag ggccacagat tggattaat gagatacgag ggttgttctt ggggtgttct 1680
tccgagtaag tgagaagggt agtggattga ctac 1714

```

## (2) INFORMATION ON SEQ ID NO. 54:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

002221 5552960

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

ctcgagccgc tcgagccgaa tcggctcgag ctgaaaaagg gctacctgac cctgtcagac 60  
 agtggggaca aggtggccgt ggaatgggac aaagaccatg gggtcctgga gtcccacctg 120  
 gcggagaagg ggagaggcat ggagctatcc gacctgattg ttttcaatgg gaaactctac 180  
 tccgtggatg accggacggg ggctgtctac cagatcgaag gcagcaaagc cgtgccctgg 240  
 gtgattctgt ccgacggcga cggcaccgtg gagaaaggct tcaaggccga atggctggca 300  
 gtgaaggacg agcgtctgta cgtgggcggc ctgggcaagg agtggacgac cactacgggt 360  
 gatgtggtga acgagaaccc ggagtgggtg aagggtggtg gctacaaggg cagcgtggac 420  
 cacgagaact ggggtgtccaa ctacaacgcc ctgcccggctg ctgccggcat ccagccgcca 480  
 ggtaacctca tccatgagtc tgcctgctgg agtgacacgc tgcagcgtg gttcttctg 540  
 ccgcgcccg cccagccagga gcgctacagc gaggaaggac gacgagcgca agggcgccaa 600  
 cctgtctgtg agcgctctcc ctgacttcgg cgacatcgct gtgagccacg tcggggcggt 660  
 ggtccccact cactgcttct cgtccttcaa gttcatcccc aacaccgacg accagatcat 720  
 tgtggccctc aaatccgagg aggacagcgg cagagtcgcc tcctacatca tggccttcac 780  
 gctggacggg cgcttctctg tgcgggagac caagatcgga agcgtgaaat acgaaggcat 840  
 cgagttcatt taactcaaaa cggaaacact gagcaaggcc atcaggactc agcttttata 900  
 aaaacaagag gactgcactt ttgttttgtt ttgttctttt tggaaactgtg cctggggttg 960  
 aggtctggac agggagccca gtcccggggc ccatagtggg gcgggcactg gacccccggg 1020  
 cccacggag gccgcggtct gaactgcttt ccatgctgcc atctggtggt gatttcgggt 1080  
 acttcaggca ttgactcaag gcctgcctaa ctggctgggt cgtttcttcc atccgacct 1140  
 gtttcttttc tttcctatgt tcttttgttc agtgaatata cctagagctc ctaccatatg 1200  
 tcaggcccta tgccctaccc tgagaacgca gtaagcatga aggtggacct ggtttgctgg 1260  
 gaaccggagg gctaaccctt tttttcttcc caaatttggt gccttgggaag aatcaggtcc 1320  
 agccctgaag atccttgggg 1340

## (2) INFORMATION ON SEQ ID NO. 55:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 765 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00673396-12700  
00673396-12700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

caggattgaa acaagatggc gggttcgtgg tgagaagccg tcaaggagta gaaattggta 60
tgcttagaag cagattctaa aagcagtttc tcttcagaac atcttttttc ataccacttg120
ataagcatct tgaaacacca tggctgtagc tgcagtaaaa tgggtgatgt caaagagaac180
tatcttgaaa catttatttc cagtccaaaa tggagcttta tattgtgttt gtcataaatc240
tacgtattct cctctaccag atgactataa ttgcaacgta gagcttgctc tgacttctga300
tggcaggaca atagtatgct accacccttc tgtggacatt ccatatgaac acacaaaacc360
tatccctcgg ccagatcctg tgcataataa tgaagaaaca catgatcaag tgctgaaaac420
cagattggaa gaaaaagttg aacaccttga ggaaggacct atgatagaac aacttagcaa480
aatgttcttt actactaagc accgttggtg toctcatgga cggtatcaca gatgtcgtaa540
gaatctgaat cctccaaaag acagatgatg cggaggttcc tgggggaatc aaagagaaat600
gtgcctcatt tgccatttga gaaaatgcag tctggtgtat tcagtaatat atagttaaagt660
aataatgata aaatatcttt tcatatatta gaatgtgtac ttttatataa agtaattctg720
gatttgacat tctcatttag ggggacctat tccttttttc gtttt 765

```

## (2) INFORMATION ON SEQ ID NO. 56:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1647 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004227 56E4960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

gcagccggag taagatggcg gcgctgaggg ctttgtgctg cttccggggc gtcgcgggcc 60
aggtgctgcg gcctggggct ggagtcgatg tgccgattca gcccagcaga ggtgttcggc 120
agtggcagcc agatgtggaa tgggcacagc agtttggggg agctgttatg tacccaagca 180
aagaaacagc cacttggaag cctccacctt ggaatgatgt ggacctcca aaggacacaa 240
ttgtgaagaa cattaccctg aactttgggc cccaacaccc agcagcgcat ggtgtcctgc 300
gactagtgat ggaattgagt ggggagatgg tgcggaagtg tgatcctcac atcgggctcc 360
tgcaccgagg cactgagaag ctcatatgat acaagacctt tcttcaggcc cttccatact 420
ttgaccggct agactatgtg tccatgatgt gtaacgaaca ggcctattct ctagctgtgg 480
agaagttgct aaacatccgg cctcctcctc gggcacagtg gatccgagtg ctgtttggag 540
aaatcacacg tttgttgaa ccatcatggt ctgtgaccac acatgccttg gaccttgggg 600
ccatgacccc tttcttcttg ctgtttgaa aaagggagaa gatgtttgag ttctacgagc 660
gagtgtctgg agcccgaatg catgctgctt atatccggcc aggaggagt caccaggacc 720
tacccttggt gcttatggat gacatttata agttttctaa gaacttctct cttcggcttg 780
atgagttgga ggagttgctg accaacaata ggatctggcg aaatcggaca attgacattg 840
gggttgtaac agcagaagaa gcaacttaact atggttttag tggagtgatg cttcggggct 900
caggcatcca gtgggacctg cggaagaccc agccctatga tgtttacgac caggttgagt 960
ttgatgttcc tgttggttct cgaggggact gctatgatag gtacctgtgc cgggtggagg 1020
agatgcgcca gtccctgaga attatcgac agtgtctaaa caagatgcct cctggggaga 1080
tcaagggtga tgatgcaaaa gtgtctccac ctaagcgagc agagatgaag acttccatgg 1140
agtcactgat tcatcacttt aagttgtata ctgagggcta ccaagttcct ccaggagcca 1200
catatactgc cattgaggct cccaagggag agtttggggg gtacctggtg tctgatggca 1260
gcagccggcc ttatcgatgc aagatcaagg ctcttggttt tgcccatctg gctggtttgg 1320
acaagatgtc taagggacac atgttggcag atgtcggttg catcataggt acccaagata 1380
ttgtatttgg agaagtagat cggtgagcag gggagcagcg tttgatcccc cctgcctatc 1440
agcttcttct gtggagcctg ttctcactg gaaattggcc tctgtgtgtg tgtgtgtgtg 1500
tgtgtgtgtg tgtgtgtatg ttcatgtaca cttggctgtc aggccttctg tgcattgtac 1560
aaaaaaggag aaattataat aaattagccg tcttgccgcc ctaggcctaa aaaaaaaaaa 1620
aaaaaaaaaa aaaaaaaaaa aaaaaaa 1647

```

## (2) INFORMATION ON SEQ ID NO. 57:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1166 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395 "122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

cgccgcctgc gcggggggga gcccagcaca gaccgcccgc gggacccoga gtcgcgcacc 60  
ccagcccccac cgcccacccc gcgcgccatg gaccccaagg accgcaagaa gatccagttc 120  
tcggtgcccg cgccccctag ccagctcgac ccccgccagg tggagatgat ccggcgagg 180  
agaccaacgc ctgccatgct gttccggctc tcagagcact cctcaccaga ggaggaagcc 240  
tccccccacc agagagcctc aggagagggg caccatctca agtcgaagag acccaacccc 300  
tgtgcctaca caccaccttc gctgaaagct gtgcagcgca ttgctgagtc tcacctgcag 360  
tctatcagca atttgaatga gaaccaggcc tcagaggagg aggatgagct gggggagctt 420  
cgggagctgg gttatccaag agaggaagat gaggaggaag aggaggatgc agccaggctg 480  
aagtcctgaa ggtcatcagg cagtctgctg ggcaaaagac aacctgtggc cagggtctgg 540  
aagggccctg ggagcgccca cccctctctg atgagtcga gagagatgga ggctctgagg 600  
accaagtgga agacccctc ctaagtgagc ctggggagga acctcagcgc ccttccccct 660  
ctgagcctgg caccagggg cccagcctgc atctcccagg aggaagtgga ggggacatcg 720  
ctgttcccca gaaacccctc ctatcctcac cctgttttgt gctcttcccc tcgcctgcta 780  
gggctgcggc ttctgacttc tagaagacta aggcctgtct gtgtttgctt gtttgccac 840  
ctttggctga taccagaga acctgggcac ttgctgcctg atgcccaccc ctgccagtc 900  
ttcctccatt caccagcgg gaggtgggat gtgagacagc ccacattgga aaatccagaa 960  
aaccgggaac agggatttgc ccttcacaat tctactcccc agatcctctc ccctggacac 1020  
aggagaccca cagggcagga ccctaagatc tggggaaagg aggtcctgag aaccttgagg 1080  
tacccttaga tccttttcta cccactttcc tatggaggat tccaagtcaa catttgtctg 1140  
aacggcttgt aacagggttc aggttg 1166

## (2) INFORMATION ON SEQ ID NO. 58:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 487 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

ctcagatcgg tggacgtgct cgctccact cggggccagg tctatgtccc ggtttcccgc 60  
agtcgcgggc agggcgccaa ggcggcagga ggagggtgag cgggtcaagag acctccaggal 120  
agagcggctc tcggctgttt gcatcgccga tagagaagag aaaggatgca cgtcccaggal 180  
gggaggaact actccaactt ttctatttca gaaacaaaga aaaaagatta ttcaagctgt 240  
gagggacaat tcattcctta ttgttactgg aaatacagga agtggtaaaa caactcaact 300  
cccaaaatat ctatatgaag caggggtttt acaacatggt atgattggtg taactcaacc 360  
acgaaaagta gctgctatat cagttgctca gagagtagct gaagaaatga aatgcacttt 420  
gggatccaaa gtaggatacc aagttcggtt tgatgattgc agttctaagg agacagcaat 480  
caaatat 487

002227-5657960

## (2) INFORMATION ON SEQ ID NO. 59:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1630 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

aaactgtgta atgccccatg taatccataa aattttaact tttcccccta acgtttttgc 60
tgaaaaatgt tgggaaaccc tcaacacgcc ttctgaaaa caattaaaat acttgaaacc 120
tgtgaacctt tcaaaaaacc ctacaggttg gaaaagaccc ccaaaccttc ttttaaggat 180
catttgtctc gcccatcaca ggatcttgga aatgtttccc taggggtgtg ttttaaggat 240
ccagggggga atgaagcaca tttttctggc aaccaaactt gagttcctca gagaacagat 300
gcagagagac ctgctcctgc ttgcccggct acagggggcca ctgtggagtc aactgaggc 360
tgtgaccggc cataagccca ggagagcccg tggcagctgt gccgaggcgc caggacctct 420
aagcgggaagc ttcccaagct aggaatggag caacactgca atgaaatgtg tccaccaagc 480
tcattgttcc tcccgggtgc ttataaaagc cagatgtata gtgacgtatg gacaaatata 540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gcctttcttt ctacacaggc taagacacaa 600
atttatatatt gttatgaagc actttttacc aacgggtcagt ttttacattt tatagctgcg 660
tgcgaaaggc ttccagatgg gagaccatc tctcttggtc tccagacttc atcacaggct 720
gcttttttcc aaaaaggggg aaactcatgc ctttcccttt taaaaaatgc ttttttgtat 780
ttgtccatac gtcactatac atctgagctt tataagcgcc cgggaggaac aatgagcttg 840
gtggacacat ttcattgcag tgttgctcca ttcttagctt gggagagctc cgcttagagg 900
tcctggcgcc tcggcacagc tgccacgggc tctcctgggc ttatggccgg tcacagcctc 960
agtgtgactc cacagtggcc cctgtagccg ggcaagcagg agcagggtct tctgcatctg 1020
ttctctgagg aactcaagtt tgggtgcccag aaaaatgtgc ttcattcccc cctgggttaatt 1080
ttttacacac cctaggaaac atttccaaga tctgtgatg gcgagacaaa tgatccttaatt 1140
agaaggtgtg ggtcttttcc caacctgagg atttctgaaa ggttcacagg ttcaatattt 1200
aatgcttcag aagcatgtga ggttcccaac actgtcagca aaaaccttag gagaaaactt 1260

aaaaatatat gaatacatgc gcaatacaca gctacagaca cacattctgt tgacaaggga 1320
aaaccttcaa agcatgtttc tttccctcac cacaacagaa catgcagtac taaagcaata 1380
tatttgtgat tccccatgta attcttcaat gttaaacagt gcagtcctct ttcgaaagct 1440
aagatgacca tcgccccttt cctctgtaca tataccctta agaacgcccc ctccacacac 1500
tgccccccag tatatgccgc attgtactgc tgtgttatat gctatgtaca tgtcagaaac 1560
cattagcatt gcatgcaggc ttcatattct ttctaagatg gaaagtaata aaatatattt 1620
gaaatgtacc                                     1630

```

00673395.122700

## (2) INFORMATION ON SEQ ID NO. 60:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

tgcgcgcgag cccgtgtccc cacggcgggc agcagcgggc gcggcgggcg ctgaacgcgg 60
agggggcgga gggagcccg ggcggcgcca gcagctacag cgaaatggcg gagaccgtgg 120
ctgacacccc gcggtgatc accaagccgc agaacctgaa tgacgcctac ggacccccca 180
gcaacttcct cgagatcgat gtgagcaacc cgcaaacggg gggggtcggc cggggccgct 240
tcaccactta cgaaatcagg gtcaagacaa atcttcctat tttcaagctg aaagaatcta 300
ctgttagaag aagatacagt gactttgaat ggctgcgaag tgaattagaa agagagagca 360
aggtcgtagt tcccccgctc cctgggaaag cgtttttgcg tcagttcctt ttagaggaga 420
tgatggaata tttgatgaca attttattga ggaaagaaaa caagggtctg agcagtttat 480
aaacaaggtc gctggtcac cctctggcaca gaacgaacgt tgtcttcaca tgtttttaca 540
agatgaaata atagataaaa gctatactcc atctaaaata agacatgcct gaaatttggc 600
aagaaggggc aaaaacgtga ctattaatga ttgataagca ccagtgaaga agttctaact 660
tttagcatgc tgcacagaaa ctggtataac atgccttcag tatactaaca ctcatatgct 720
cagttttgtt ttgttttggc agttgacaag aagttaattt gcttttagtaa aaatccctca 780
ttccagcctt tctatataaa tagctctttc ttgctgtttt aatgtggtgc acactatagc 840
ctcaciaaac tgttattcca gtgtaatctg cagtgtcgtg actaaagtta ctggcttggc 900
cttatttgca cagtttttgc gtcttgtttg cttcttgcat ctgattaact agaataattc 960
tctttccccc ttttaatttg tgatgtcact tgacccatt tatgtgtagg agcactacac1020
cattggtttc caatactgca cacataagat acatacttgt gtgcagaaaag tatcttcctc1080
caggcttgta ataccettca catggaagat taatgagga aatctttata ttctgtataa1140
aaacaaaagc aaatttatat actaaaatca tttgtctaaa aatttaagtt gttttcaaat1200
aaaaattaaa atgcatttct gatatgcaaa aaaaaaaaaa aagaaaaaga aaaaaagagg1260
ggcgccgct ct                                     1272

```

004221"5652960



## (2) INFORMATION ON SEQ ID NO. 61:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1914 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```

tgcagcgcgt gcggtgctgcg ctactgagca ggcgccatgga ggactctgaa gcaactgggct 60
tcgaacacat gggcctcgat ccccggtctc ttcaggctgt caccgatctg ggctgggtcgc 120
gacctacgct gatccaggag aaggccatcc cactggccct agaagggaag gacctcctgg 180
ctcgggcccc caggggctcc gggaagacgg ccgcttatgc tattccgatg ctgcagctgt 240
tgctccatag gaaggcgaca ggtccggtgg tagaacaggc agtgagaggc cttgttcttg 300
ttcctaccaa ggagctggca cggcaagcac agtccatgat tcagcagctg gctacctact 360
gtgctcgga tgtccgagtg gccaatgtct cagctgctga agactcagtc tctcagagag 420
ctgtgctgat ggagaagcca gatgtggtag tagggacccc atctcgcata ttaagccact 480
tgcagcaaga cagcctgaaa cttcgtgact ccctggagct tttgggtggg gacgaagctg 540
accttctttt ttcttttggc tttgaagaag agctcaagag tctcctctgg gaaggcagag 600
tcacttgccc cggatttacc aggtttttct catgtcagct acttttaacg aggacgtaca 660
agcactcaag gagctgatat tacataacct ggttaccctt aagttacagg agtcccagct 720
gcctgggcca gaccagttac agcagtttca ggtggtctgt gagactgagg aagacaaatt 780
cctcctgctg tatgccctgc tcaagctgtc attgattcgg ggcaagtctc tgctctttgt 840
caacactcta gaacggagtt accggctacg cctgttcttg gaacagttca gcatccccac 900
ctgtgtgctc aatggagagc ttccactgcg ctccagggtg cacatcatct cacagttcaa 960
ccaaggcttc tacgactgtg tcatagcaac tgatgctgaa gtctggggg cccagtcacaa 1020
gggcaagcgt cggggccgag ggcccaaagg ggacaaggcc tctgatccgg aagcaggtgt 1080
ggcccggggc atagacttcc accatgtgtc tgctgtgctc aactttgatc ttcccccaac 1140
cctgaggcc tacatccatc gagctggcag gacagcacgc gctaacaacc caggcatagt 1200
cttaaccttt gtgcttccca cggagcagtt ccacttaggc aagattgagg agcttctcag 1260
tgagagaaac aggggccccca ttctgctccc ctaccagttc cggatggagg agatcgaggg 1320
cttcgcgtat cgctgcaggg atgccatgcy ctcagtgaat aagcaggcca ttcgggaggc 1380
aagattgaag gagatcaagg aagagcttct gcattctgag aagcttaaga catactttga 1440
agacaacctt agggacctcc agctgctgcy gcatgacctt cctttgcacc ccgcagtgg 1500
gaagccccac ctgggccatg ttcttgacta cctggttctt cctgctctcc gtggcctgg 1560
acgccctcac aagaagcgga agaagctgtc ttctcttgtt aggaaggcca agagagcaaa 1620
gtcccagaac ccaactgcga gcttcaagca caaaggaaa aaattcagac ccacagccaa 1680
gccttctga ggttgttggg cctctctgga gctgagcaca ttgtggagca caggcttaca 1740
cccttcgtgg acaggcgagg ctctggtgct tactgcacag cctgaacaga cagttctggg 1800
gccggcagtg ctgggccctt tagctccttg gcacttccaa gctggcatct tgccccttga 1860
caacagaata aaaatttttag ctgccccaaa aaaaaaaaaa aaaaaaaa aaaa 1914

```

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 62:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 608 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

aatggaacca ggaattctta attaagcccg aagttcccaa gtctccttag cggaaaccgg 60
aaattgcccc aggaaagcaa agagggagat gaccagtgat acctccagtg ccagagggtca120
ctttgtggag ccaaatgcgt gacatgggca gtcgagactc ggcatcttct gtcccccgca180
ttaatgactc tcaggaagga ggatgtaatt caaggcaagt ttctaattcc gaagctgcct240
gttcattgta acaggacttc tttttattcg tcaagatgta ctgggtccct ggcaccttaa300
gggaaatcct gataaaggca aacctgttga gccatttggt cccataggat cccaggaccc360
aagtccctgtg tttcatcggt actaccatgt gttccgtgag ggagaactgg aagggtgcctg420
caggactgtg agtgatgtca gaattctgca aagctactac gatcaaggaa actgggtgtgt480
gattcttcaa aaggcctgat tatttacctg aacacatcat atataaagaa gaaatgctca540
cttaaaaaaa aaagagggga taaattaatt acccgtttaa ttaaagagaa aacttgtggg600
gaagtacc                                     608

```

## (2) INFORMATION ON SEQ ID NO. 63:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2674 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

00673395.12700

## (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

tgaagagaag ttaaggtgaa gagccgaaga gcctgatgcg tgatgagcgt ctaagaaagg 60
agaagcaaga gcagagaaga gagagagaaa gaacgggaga gagaaaaggga agaaagagaa 120
aggaaaagac gaagggaaga ggaagaaaaga gaaaaagaaa gggctcgtga cagagaaaaga 180
agaaagagaa gtcgttcacg aagtagacac tcaagccgaa catcagacag aagatgcagc 240
aggtctcggg accacaaaaag gtcacgaagt agagaaaaga ggcggagcag aagtagagat 300
cgacgaagaa gcagaagcca tgatcgatca gaaagaaaac acagatctcg aagtcgggat 360
cgaagaagat caaaaagccg ggatcgaaaag tcatataagc acaggagcaa aagtcgggac 420
agagaacaag atagaaaatc caaggagaaa gaaaagaggg gatctgatga taaaaaaagt 480
agtgtgaagt ccggtagtgc agaaaagcag agtgaagaca caaactctga atcgaaggaa 540
agtataacta agaatgaggt caatgggacc agtgaagaca ttaaactctga aggtgacact 600
cagtccaatt aaaactgatc tgataagacc tcagatcaga cagaggtaaag tgtattgttt 660
ctcactttga ttagggtctt ttgttactgt ttgacagtgc agcgtaaagta tgcacagatg 720
aagatggaac taagccgagt aagaagacat acaaaaagcct cttctgaagg aaaagacagt 780
gtagtccctgc aaaacatttt gaggtacatt gttttgtctc agctattttg tagcagactc 840
gtgcccccat tagtgtgcct ctttggaat tatcgccac atttgtaata tagtcgcat 900
tgaaaagtta attatccttt ttttagggat tttgatgtca tttctttttt ttttttaata 960
aaaaggttga actgtttttt ttttctttt tggatattaag tccatcttgt gttggtacat 1020
tggcagagac atatgcttta aaaacttaaa tatttcggag gcacatgttg gactactttg 1080
ttttaattaa actgctagta tttctttgtc aaggatgttt ctagtttttt gctttattgc 1140
cttgcatctt aatgcagttt gttctgtaac tcgagagcca gtagcattgg attgatggaal 1200
gtgtagggtt tatgaattat tgcagctgac taccatacct cacacagcgt tgggtgtgtg 1260
agcggcccat gaaaagccaa attaaaaatc aaggattcag tcaaactaag cagggtactcal 1320
tgccaggtaac tcctttctct acccacatcc atgtttgaat gctattgcct gtgatcttta 1380
cgcttaactg ttgtgtatct tttttgttct ttacaagaag tgcagagggg tttttgtgt 1440
attgcgtgaa aacttataaa acaaattgta acagaatgga attttttttc aactgtatgt 1500
agggctgcag tgggtggccag aattagatat ctttaagaa ttttaaatat aataaacact 1560
tcatattatt cgccttggtt cactcaatgc aattctcaag tctataagag gtatgtgctt 1620
aatatttcct actgtgtagg agaatttgca gtcagccata ggtatgtagg aatagtcact 1680
cactggctga tacattttaa gcagcagtggt gaatagcaag gacagacacc ttcaatttgt 1740
gaaatcaaag aactgatgca ctatatagaa cgaatttggt tttttaaaga aatattaaaa 1800
gttaggtact gtaagtgttc ttaaaacctg taaacttcat tctgtgggct agtgggtgg 1860
gacaaaatat tcctaataa aggaagtacc aattagttga tttgttggtg gcattcccct 1920
tttgggaaag caatgtaagg ttatgtctgt gtatgtcatt cacacttagg caagcatacal 1980
caggcacatg gctttaagaa ccacactgat gccttgataa ttaaaaagaa tacaagcatt 2040
ccatgtacac atgttaatta gcagttagtg actgggcca cactttctca taaaaattgg 2100
ccttttacat gttgtctaata tatcattttt ccccaaattt tgcgttgtag gactactgtt 2160
cgaagatttt tggagaataa ctgagaacgg cataaagtga agatcgacat ttaaaaaatg 2220
aggtgaaaga aagctatagt ggcatagaaa aagtataaag ctcagttagt tttttatta 2280
ttattattat taaaagttaa ttcaggactg atgtgacctt ccagatttca gaacatgtgt 2340
taatagtata tatgccactg aaaacttagg tcctgtatca tacttttttc ttttaagact 2400
tttaagaaat attacttaaa catgtggctt gctcagtggt taattgcaag ttttcaatct 2460
tggactttga aaacaggatt aaacgttagt attcgtgtga atcagactaa gtgggatttc 2520
atttttacaa ctctgctcta cttagccttt ggatttagaa gtaaaaaata agtatctctg 2580
actttctgtt acaaagttga ttgtctctgt cattgaaaag ttttagtatt aatctttttc 2640
taataaaagt attgactctg aaaaaaaaaa aaaa

```

2674

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 64:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 326 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

gacaaatgag ggtttggcat gcagctcgtc atcttaagag ttactatctt cttgccctgg 60
tgtttcgccg ttccagtgcc cctgctgca gaccataaag gatgggactt tgttgagggc120
tatttccatc aatttttcct gaccgagaag gagtcgccac tccttaccga ggagacacaal80
acacagctcc tgcaacaatt ccatcggaat gggacagacc tacttgacat gcagatgcat240
gcttctgcta cagcagcccc actgtggggg gcctgatggg tccgacaact gcatctcgcc300
aggaagatgc aagtggatta agcaca                                     326

```

## (2) INFORMATION ON SEQ ID NO. 65:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 888 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227"56E/960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```

ctcgtgcggt gatgttgagc agaagataca attcaaaaaga gaaacagcca gtttgaaaact 60
gttaccacac cagccccgaa ttgtggagat gaagaaagga agcaatggct atgggtttcta120
tctgagggca ggctcagaac agaaaggta aatcatcaag gacatagatt ctggaagtcc180
agcagaggag gctggcttga agaacaatga tctggtagtt gctgtcaacg gcgagtctgt240
ggaaaccctg gatcatgaca gtgtggtaga aatgattaga aagggtggag atcagacttc300
actgttggtg gtagacaaag agacggacaa catgtacaga ctggctcatt tttctccatt360
tctctactat caaagtcaag aactgcccac tggctctgtc aaggagggtc cagctcctac420
tcccacttct ctggaagtct caagtccacc agatactaca gaggaagtag atcataagcc480
taaactctgc aggctggcta aagggtgaaaa tggctatggc tttcacttaa atgcgattcg540
gggtctgcca ggctcattca tcaaagaggt acagaagggc ggtcctgctg acttggtgg600
gctagaggat gaggatgtca tcattgaagt gaatggggtg aatgtgctag atgaacccta660
tgagaagggt gtggatagaa tccagagcag tgggaagaat gtcacacttc tagtctgtgg720
aaagaaggcc tatgattatt tccaagccta agaaaatccc tattgttccc tgcctggctg780
atgccagttg acagccctgc aggttctaaa gaaggaatag tggtgagtc aaaccatgac840
tcgcacatgg caaaagaacg ggcggctatt gcagacggct aatttatg 888

```

## (2) INFORMATION ON SEQ ID NO. 66:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 202 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```

atcacagggg tacaaccaga acacatacag tacttgaaaa attatttcca ctttggaca 60
cgacagttag cgcataattta tcaactactat attcatggcc caaaaggaaa tgaaatacga120
acatcaaaaag aagttgaacc tttcaacaat attgatattg aaatttctat gtttgaaaaa180
gggaagggtac ctaagattgt ca 202

```

09673395-122700

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1225 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

ggcgcggtgga	ggcggcgggct	gcgggcacgga	aggggaagcgc	ctgagggcggg	ggggcccaca	60
gccatggcgg	agctgtgtgca	ggaggagctc	tcgggtcctgg	ccgcgattttt	ctgcaggccc	120
cacagatggg	aggtgctgag	ccgctcagag	acagatggga	ccgtgttcag	aattcacaca	180
aaagctgaag	gatttatgga	tgcggatata	cctctggaat	tggtgttcca	tttgccagtc	240
aattatcctt	catgtctacc	tggtatctcg	attaactctg	aacagttgac	cagggcccag	300
tgtgtgactg	tgaaagagaa	gttacttgag	caagcagaga	gccttttgtc	ggagcctatg	360
gttcatgagc	tggttctctg	gattcagcag	aatctcaggc	atatcctcag	ccaaccagaa	420
actggcagtg	gcagtgaaaa	gtgtactttt	tcaacaagca	cgaccatgga	tgatggattg	480
tggaataactc	ttttgcattt	agatcacatg	agagcaaaga	ctaaatatgt	caaaatttgt	540
gagaagttggg	cttcagattt	aaggctgaca	ggaagactga	tggtcatggg	taaaataata	600
cttgattttta	ctacagggag	acagaaacaa	cctcaagggtg	tacttgattc	ttcagaaaac	660
ctccaaagta	gatgtggact	caagtggaaa	gaaatgcaaa	gagaaaatga	ttagtgtact	720
gtttgaaaca	aaagtacaga	cagaacacaa	aaggtttctg	gcatttgaag	tcaaagagta	780
ttcagcgttg	gatgaattac	aaaaggaatt	tgaaactgca	ggacttaaga	agctttttctc	840
cgaatttgta	cttgctctgg	taaaatgaaa	tgggaagacag	gaatctttta	gtaaaaatagc	900
agtgtttttt	gttggttttg	cattggattt	ggggagtggg	taattgaaat	agtcaatttt	960
aaagttttctc	tgaagcaaaa	tgataggcat	cattctaact	tcaggaacaa	acgccagttc	1020
tgtttttatga	aataattaaac	atgaagaaaa	cttgtatat	ctaattgttg	ccaggaagg	1080
ctaggttcag	tagatgagac	attattttaaa	agataaattt	aaaaagatgg	taaatgaaca	1140
cttgttttta	tagacaatat	ttgtttgaaa	ctatgtaatt	ttctggctaa	ttttcttgta	1200
attaaatgat	tttttaaaaa	aagaa				1225

(2) INFORMATION ON SEQ ID NO. 68:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1093 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

gagggcgggc ctgtttccgg ggaggcgcggt ggggcttgag gccgagaacg gcccttgctg 60
ccaccaacat ggagactttg taccgtgtcc cgttcttagt gctcgaatgt cccaacctga 120
agctgaagaa gccgccctgg ttgcacatgc cgtcggccat gactgtgtat gctctggtgg 180
tgggtgtctta cttcctcatc accggaggaa taatttatga tgttattggt gaacctccaa 240
gtgtcggttc tatgactgat gaacatgggc atcagaggcc agtagctttc ttggcctaca 300
gagtaaatgg acaatatatt atggaaggac ttgcatccag cttcctattht acaatgggag 360
gttttaggttt cataatcctg gaccgatcga atgcaccaa tatcccaaaa ctcaatagat 420
tccttcttct gtccattgga ttctgtctgt tctatttagg ttttttcatg gctagagtat 480
tcatgagaat gaaactgccg ggctatctga tggggttagag tgcctttgag aagaaatcag 540
tggatactgg atttgtctct gtcaatgaag ttttaaaggc tgtaccaatc ctctaatatg 600
aaatgtggaa aagaatgaag agcagcagta aaagaaatat ctagtgaaaa aacaggaagc 660
gtattgaagc ttggactaga atttcttctt ggtattaaag agacaagttt atcacagaat 720
tttttttctt gctggcctat tgctatacca atgatgttga gtggcatttt ctttttagtt 780
tttcattaaa atatattcca tatctacaac tataatatca aataaagtga ttatttttta 840
caaccctctt aacatttttt ggagatgaca tttctgattt tcagaaatta acataaaatc 900
cagaagcaag attccgtaag ctgagaactc tggacagttg atcagcttta cctatggtgc 960
tttgccttta actagagtgt gtgatggtag attatttcag atatgtatgt aaaactgttt1020
cctgaacaat aagatgtatg aacggagcag aaataaatac tttttctaata taaaaaaaaa1080
aaaaaaaaaa aaa                                     1093

```

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 309 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

002227 5656950

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

cacaaagtga ttgtggtatg gaacaatatt ggagagaagg caccagatga gttatggaat 60
tctctagggc cccaccctat cctgtgtatc ttcaaacaac agacagcaaa caggatgaga120
aatcgactcc aggtctttcc tgaactggaa accaatgcag tgttgatggt agatgatgac180
acactcatca gcaccccgaga ccttggtttt gctttctcag tttggcagca atttcctgat240
caaattgtag ggatttgttt cctagaaagc acgtctttta ctttcattca aggtatctac300
agttattgg
309

```

## (2) INFORMATION ON SEQ ID NO. 70:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 380 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```

ctcatctgat cccttttatg gccaaatcat ccttcagagt agggaaacact cagacattct 60
gtgcatgttg ttcccccaaa gcatggtcat cacaaagtcc tgagttctgg tgtgtgctcc120
cgctcctggt gtatacagag agaaggcagg aatcaggagt tccagaagca tatacatgtg180
gctaccccag caacaagcgg catcctgtgc tcagataagc tgcattggtt ggaagtgttt240
ttcctcgac gttgaggctt agtggagatg ggcaccactg ccatttgctc agaagaaggc300
tggtctggtc ctaactgcat cccacactgc ccagatcatt ctagataggt tatttttctga360
atgtttatag atttcttata
380

```

## (2) INFORMATION ON SEQ ID NO. 71:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1253 base pairs

00422T"56E2960



(B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

gcggcccgac tccagttagg agccttgatg ccggagggga cagtgggtcg ccgagagcgc 60  
 ccggagggaa ccgcctggcc ttcggggacc accaattttg tctggaacca ccctcccggc 120  
 gtatcctact ccctgtgccg cgaggccatc gcttacttgg aggggtcgat ttgtgtgtag 180  
 tttggtgaca agatttgcat tcacctggcc caaacccttt ttgtctcttt ggggtgaccgg 240  
 aaaactccac ctcaagtttt cttttgtggg gctgcccccc aagtgtcggt tgttttactg 300  
 tagggctctc ccgcccggcg cccccagtggt tttctgaggg cggaaatggc caattcgggc 360  
 ctgcagttgc tgggcttctc catggccctg ctgggctggg tgggtctggt ggccctgcacc 420  
 gccatcccgc agtggcagat gagctcctat gcgggtgaca acatcatcac ggcccaggcc 480  
 atgtacaagg ggctgtggat ggactgcgtc acgcagagca cgggggatgat gagctgcaaa 540  
 atgtacgact cgggtgctgc cctgtccgcg gccttgccagg ccactcgagc cctaattggtg 600  
 gtctccctgg tgcctgggctt cctggccatg tttgtggcca cgatgggcat gaagtgcacg 660  
 cgctgtgggg gagacgacaa agtgaagaag gcccgatatg ccatgggtgg aggcataatt 720  
 ttcactcgtg caggtcttgc cgccttggtg gcttgcctct ggtatggcca tcagattgtc 780  
 acagactttt ataacccttt gatccctacc aacattaagt atgagtttgg ccctgccatc 840  
 tttattggct gggcagggtc tgccctagtc atcctgggag gtgcactgct ctccctgttcc 900  
 tgtcctggga atgagagcaa ggctgggtac cgtgcacccc gctcttacc taagtccaac 960  
 tcttccaagg agtatgtgtg acctgggatc tccttgcccc agcctgacag gctatgggag 1020  
 tgtctagatg cctgaaaggg cctggggctg agctcagcct gtgggcaggg tgccggacaal 1080  
 aggcctcctg gtcactctgt ccctgcactc catgtatagt cctcttgggt tgggggtggg 1140  
 ggggtgccgt tgggtgggaga gacaaaaaga gggagagtgt gctttttgta cagtaataaaa 1200  
 aaataagtat tgggaaacaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1253

(2) INFORMATION ON SEQ ID NO. 72:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 439 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

00673395-122700

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

ctaaggggag gacaggcaga aaccaggaat gccaaacttaa acctgtttgg tgctctgact 60
gtttgttagt atcaactctca agaatgaaga gaaacctcaa cctttctgtt tccggccaac120
tttattgaat ttgttttttt aaatgcagtt tacatgcagt ttctttgaaa agtcatgttg180
aatntagatc tgttctctga gtaagacttg gcgagtatgt gaaacttgac tcaagttaca240
tttctttttt tctgtccccc aaacgttcac gcttcttata ggctccactt tgaggctctg300
atgaacattc cagtgtctgg gttggatgtc aatgatgatt ttgctgagga agtaacaaaa360
caagaagacc tcatgagaga ggtgggaagg actttaactc ctgtttttct ggtggtttcc420
ctttggttgt accttttaa

```

(2) INFORMATION ON SEQ ID NO. 73:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1252 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

002227"5652960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

tggacctgcc cgacgccctg ctgcccgaact tgcccgcgct ggtgggcccc aagcagctga 60
tcgtgctggg aaacaaagtg gacctcctgc cccaggatgc tcctggctac cggcagaggc 120
tgcgggagcg actgtgggag gactgtgccc gcgcccgggt cctgctggcc cctggcacca 180
agggccacag cgccccgtca aggacgagcc acaggacggg gagaatccga atccgccgaa 240
ctggtcccgc acagtgttca gggacgtgcg gctgatcagc gccaaagaccg gctatggagt 300
ggaagagttg atctctgccc ttcagcgctc ctggcgctac cgtgggggacg tctacttagt 360
gggcgccacc aacgccggca aatccactct cttaaacacg ctctggagt ccgattactg 420
cactgccaaag ggctccgagg ccatcgacag agccaccatc tccccttggc caggtactac 480
attaaacctt ctgaagtttc ctatttgcaa cccaactcct tacagaatgt ttaaaaggca 540
tcaaagactt aaaaaagatt caactcaagc tgaagaagat cttagtgagc aagaacaaaa 600
tcagcttaat gtccctcaaaa agcatggtta tgcgttagga agagttggaa ggacattctt 660
gtattcagaa gaacagaagg ataacattcc ctttgagttt gatgctgatt cacttgcctt 720
tgacatggaa aatgaccctg ttatgggtac acacaaatcc accaaacaag tagaattgac 780
tgcacaagat gtgaaagatg cccactgggt ttatgacacc cctggaatta caaaagaaaa 840
ttgtatttta aatcttctaa cagaaaaaga agtaaatatt gttttgccaa cacagtccat 900
tgttccaaga acttttgtgc ttaaaccagg aatggttctg tttttgggtg ctataggccg 960
catagatttc ctgcagggaa atcagtcagc ttggtttaca gtcgtggctt ccaacatcct 1020
ccctgtgcat atcacctcct tggacagggc agacgctctg tatcagaagc atgcaggtca 1080
tacgttactc cagattccaa tgggtggaaa agaacgaatg ggcaggattt cctcctcttg 1140
ttgctgaaga cattaatggt taaaagaaag gactgggggc aacctggaag cagtgggccg 1200
acatcaaagt ttcctctgca ggtaatttta tgccaagcac tttttaaaaa gt 1252

```

## (2) INFORMATION ON SEQ ID NO. 74:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 695 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227-5662960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

tggttcattgc ctcttgagcg tagtccagtt actttcaggc tcgggggagtg aaggcctcgt 60
tgagagaagg tctcattcgg tgttttggga agagagtcgt gtggggcccag gtatcgtagc120
ggcgacacga gagagacggg cgggtgtgaca gccttccact acctgcacga gtgtattggt180
ctgtctgcta tcagctatgc cgctgcccgt tgcgctgcag acccgcttgg ccaagagagg240
catcctcaaa catctggagc ctgaaccaga ggaagagatc attgccgagg actatgacga300
tgatcctgtg gactacgagg ccaccagggt ggagggccta ccaccaagct ggtacaaggt360
gttcgaccct tcctgcgggc tcccttacta ctggaatgca gacacagacc ttgtatcctg420
gctctcccca catgacccca actccgtggt taccaaatcg gccaaagaagc tcagaagcag480
taatgcagat gctgaagaaa agttggaccg gagccatgac aagtcggaca ggggccatga540
caagtcggac cgcagccatg agaaactaga cagggggccac gacaagtcag accggggcca600
cgacaagtct gacagggatc gagagcgtgg ctatgacaag tccaggaacg ggattcggga660
ccgcgggtat gaccaagcag accgggaaga gggcc 695

```

## (2) INFORMATION ON SEQ ID NO. 75:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2514 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004227"56E2960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```

cggcgacggc gcggggggcag ctgggaatcc ggaatgctgc ccgatggccc tgggtcctcg 60
ctgtgggggca atccgggctt gcagacgagt tttagaaaga gcgttttcgc tacgtaaagc 120
acattcgata aaggatatgg aaaatacttt gcagctggtg agaaatatca tacctcctct 180
gtcttccaca aagcaciaaag ggcaagatgg aagaataggc gtagttggag gctgtcagga 240
gtacactgga gccccatatt ttgcagcaat ctcagctctc aaagtgtgac agccccaatg 300
ctgttcatga ggtggagaag tggctgcccc ggctgcatgc tcttgctgta ggacctggct 360
tgggtagaga tgatgcgctt ctcaaaaatg tccagggcac tttggaagtg tcaaaaggcca 420
gggacatccc tgttgtcatc gacgcggtga gttgacttct ctctcctgg ctcggactcc 480
cggaaggcct gtgcagtga cagcgtcctt tgttctgtgc aggatggcct gtggtaggtc 540
gctcagcagc cggccctcat ccatggctac cggaaggctg tgctcactcc caaccacgtg 600
gagttcagca gactgtatga cgctgtgtc agaggcccta tggacagcga tgacagccat 660
ggatctgtgc taagactcag ccaagccctg ggcaacgtga cgggtgtcca gaaaggagag 720
cgcgacatcc tctccaacgg ccagcaggtg cttgtgtgca gccaggaagg cagcagccgc 780
aggtgtggag ggcaagggga cctcctgtcg ggctccctgg gcgtcctggt acaactgggcg 840
ctccttgctg gaccacagaa aacaaaatggg tccagccctc tctggtggc cgcgtttggc 900
gctgctctc tcaccaggca gtgcaaccac caagccttcc agaagcacgg tcgctccacc 960
accacctccg acatgatcgc cgaggtgggg gccgccttca gcaagctctt tgaaacctga 1020
gcccgcgcag accagaagta aacaggcacc ttggacgggg gagagcgtgt gtgtgatggg 1080
aaaatccgga cccacgcgtg tgctgaaggc gtacggtgct tgccagattt tcaacttgag 1140
cataaattgg ttgccattga gaatttaaga atctggaata ttgcagcttt tgggttaaact 1200
taatgcatgg ttggagatgt tatggcgaca ctaaaacaaag tattcctgaa ctttccttag 1260
ctccttggtg gtaactggga agacagaaat gaagaaaatc acatgagaat gaagaattct 1320
ttagcagctc aacagagttt ctggccctgc tcccagatcg gcgaagtttc tacttgttac 1380
tctctctgce ggcgcccttc gtctctctc tgettcctt ccctagtctt tcctccggca 1440
gggagctggg caggggtccc cggtgtctc cctgagtcce gactgcactg actgggtcca 1500
tcagagggct gcttcgttct ccagctcatc ttctttttaa gtggtgacta ctttggtggt 1560
atctggctgc tgggtgttgg cttattgaca tactccaggg taatcaatga tgactttggt 1620
tggaaccctt tttggaggca ccatgggaac agaaggaaac atgagtgaag ctgacccttg 1680
agtgtgtggg tggggagctc tgagacgcct cctgtcccac gctctccggt gtccgtgtct 1740
acacaggggt ccccatgata cccaccggcc ccagcagggc agaccggacc ggggacgggc 1800
acggtgaagg gctgcagcct ggggtctgac gtggccctta gtgctgtctc aggagaaggc 1860
tctggaggac ttgaggcatg ctgggcctgg tgcaagtatg gcgctaagga gaccggggga 1920
aagacagtat cgtggtcacg tatgcttagg aagcagcaca gccgtgtcct tagggatggt 1980
cgcgctccag aaagacactg gtaactgcgg tttcagccaa cactcttcat ggcaagtgtc 2040
acctcgggtt agcttctgtt gtctttgtgg atggttttcc tggagcggcc tgacgttgac 2100
gtgttctctg gtcccatgtc tttagcgggc ttctttttaa ttcgtgcctg acgctgcat 2160
tagggtgttc tcttatactt tcagtagcat ctttccacag caaggcccaa accctcctgg 2220
ttcccttcag agtctttttg gcctgatgat gactcttgag tgataccctg tgatgcagac 2280
atgccccaga tggattctac tttcttttaa actagggact ttcaagatta aaaaaaagat 2340
tgtcactact aatttgacgc ctaacttcag aagcttcact gtctacatgt gaacttttcc 2400
agaaaaactg tgccatggac atttttcctc tggggaatta acatctaaat tctggttaact 2460
attaaaaagac agatctggtt aatttaaaaa aaaaaaaaaa aaaaaataaa aaaa 2514

```

0967395-12700

## (2) INFORMATION ON SEQ ID NO. 76:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 274 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```
cagagatctg ctgtgattat tccttttcac aaaccacaat gactctggaa aacctggctg 60
taaacaccag cactgccacc agctaaggat ctgtgatcag gagtgccatc tcacggtaac120
aggcagaaga caaaagtgaa accgggctga tgcgaatcac tgggaaactg gctttggcac180
ctccagagaa tgaactgttt catagcctag ctgaccatcc atgaaaatgg ctgcctggag240
aggcagtgat cagcccatcc cctgcaagggt gaag 274
```

## (2) INFORMATION ON SEQ ID NO. 77:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 449 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002221 562960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

cgggttttagc ggcagctctt cgggattggt tccattgcca ccctaaccgt gctggcctat 60  
 gaacggtaca ttcgcgtggt ccatgccaga gtgatcaatt tttcctgggc ctggagggcc120  
 attacctaca tctggctcta ctcaactggcg tgggcaggag cacctctcct gggatggaac180  
 aggtacatcc tggacgtaca cggactaggc tgcactgtgg actggaaatc caaggatgcc240  
 aacgattcct cctttgtgct tttcttattt cttggctgcc tgggtggtgcc cctgggtgtc300  
 atagcccatt gctatggcca tattctatat ttccattcga atgcttcgtt ggtgtggaag360  
 atcttcagac aattcaagt atcaagattt taaaatatga aaagaaactg gccaaaatgt420  
 gcttttaatg atattcacct tctggtcg 449

## (2) INFORMATION ON SEQ ID NO. 78:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 346 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

atataacatc tgaattggga gatagctcat tgtggcctgg gtgctggact tttcatatta 60  
 agtctgtct tagccaaggg agaagaatgt aaggataaga ccaccaatat cacaggggct120  
 gtctgagcct ttacctgtga ttttgtacca ctctgtggcc ttctggagca atggacaacc180  
 aagtcagcta tgcagttcat aaaagtggac ctggttatat gtcattccaac agcatatggt240  
 ccctgcaagc ctgttttgga agccaatatt ctataaccta caggaatcca cttgaatctg300  
 atgtcttttg aagcaatata ttttcccagg gttccaatgg actacg 346

## (2) INFORMATION ON SEQ ID NO. 79:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1329 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

00/22T"56E/960

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```

ccccatca gttcgaattt ctgcagtga agcatctggg gttattgtga ccaactgaaa 60
gtctcagaga gtacccacgt gctccagccc ttcctcccca gcatccttga tggcttaatt 120
cacctagcag ccaggttcag ctccagaggtc ctcaacctgg tgatggagac cctgtgcata 180
gtttgtacag tagaccccg attcacagca agcatggaaa gcaaaatctg ccccttcacc 240
atcgccattt tcctaaagta cagtaatgat cccgtcgtcg cctcactggc tcaggacata 300
ttcaaggagc tgtcccagat tgaagcctgt cagggcccaa tgcaaataag gctgattccc 360
actctggtca gcataatgca ggccccagca gacaagattc ctgcagggtt ttgtgcgaca 420
ccattgatat cctgacaaca gtagtacgaa atacaaagcc tcccctttcc cagcttctca 480
tctgccaaagc tttccctgct gtggcacagt gtacccttca cacagatgac aatgccatca 540
gtgcagaatg ggggagagtg cttgcggggc tatgtgtcag tgaccctgga acaagtagcc 600
cagtggcatg atgagcaggg ccacaatgga ctgtggtatg tgatgcaagt ggtgagccag 660
ctcctggacc cccgcacctc agagttcact gcggcctttg tgggcccgcct tgtttccacc 720
ctcatctcca aggcaggcg ggaactcggg gagaatctag accagattct tcgtgccatc 780
ctcagtaaga tgcagcaggc agagacgctc agtgtcatgc agtccctgat catggtgttc 840
gctcatctgg tgcacactca gctagaacct ctcttgagtg tctgtgttag cctcccagga 900
cctactggca aacctgctct agagtttgtg atggctgagt ggacaagccg acagcacctg 960
ttctatggac agtatgaagg caaagtcagc tctgtggcac tctgtaagct gctccagcat 1020
ggcatcaatg cagatgacaa acggctacag gatatccgtg tgaagggaga ggagatctac 1080
agcatggatg agggcatccg caccgcctct aagtcagcca aaaaccaga acgctggaca 1140
aacattcctt tgctggtcaa gatcctaaag ctgatcatca acgagctctc caacgtcatg 1200
ggaggctaatt gccgctccgc caggccactc ctgcagagtg ggagtcaaag gtgcacgaag 1260
gccccttact tcccaggaag acttttagcc tgggcagatc aagttacaaa ttgtcaaatt 1320
atccaggaa 1329

```

(2) INFORMATION ON SEQ ID NO. 80:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 805 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:



(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

gcccccatca gttcgaattt ctgcagtga agcatctggg gttattgtga ccaactgaaa 60
gtctcagaga gtacccacgt gctccagccc ttctcccca gcatccttga tggcttaatt120
cacctagcag ccaggttcag ctcaaggtc ctcaacctgg tgatggagac cctgtgcatc180
gtttgtacag tagaccccg aattcacagc agcatggaaa gcaaaatctg ccccttcacc240
atcgccattt tcctaaagta cagtaatgat cccgtcgtcg cctcactggc tcaggacatc300
ttcaaggagc tgtcccagat tgaagcctgt cagggcccaa tgcaaatgag gctgattccc360
actctgggtc gcataatgca ggccccagca gacaagattc ctgcagggct ttgtgcgaca420
cccattgata tcctgacaac agtagtacga aatacaaagc ctcccctttc ccagcttctc480
atctgccaa gctttccctgc tgtggcacag tgtacccttc acacagatga caatgccacc540
atgcagaatg gcgagagtg cttgcggggc tatgtgtcag tgaccctgga acaagtagcc600
cagtggcatg atgagcaggg ccacaatgga ctgtggtatg tgatgcaagt ggtgagccag660
ctcctggacc cccgcacctc agagttcact gcggcctttg tgggccgcct ttgtttccac720
cctcatctcc aaggcagggc gggaactcgg ggagaatcta gaccagattt cttcgtgcca780
tccttcagtt aagatggcag gaggt                                     805

```

(2) INFORMATION ON SEQ ID NO. 81:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 420 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

```

accagggtcaa gctcacccca aactattacc ttcatgcat gtgttgtcat accctgtgga 60
gatctccaaa gtcaaaagca actgtcagac tcagagaagt atctgtgccc ctttaagata120
aaaggctccc cctatcaaga cccttggttc ttaacgaatg caggaaaaca ggtctgccat180
agctggaatg aggtggtgtg gacaactgaa tatcaaggct ggacctcgtc aaccggtggt240
tgtatgtcct taaaaccata cattcacttc actaaagaaa gtacccccca taattgccag300
tataaccaat gtaatccagt gcaaatttct attctcattc caacttctac tgaccctaaa360
cctacttttaa gttgcggtat atggcatggg agccgaaata gcaggggcac atcttattgg420

```

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## (2) INFORMATION ON SEQ ID NO. 82:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2143 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227" 56EE2960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

cgggcgcgcct tttttttttt ttttttaagt tgaacagaac attttatttc tcagcaattc 60
tatgcgtaca aattaaacat gagatgaata gagactttat tgagaaagca agagaaaatt 120
cctatcaacc ccaaggagga ctcaaagtga ggctggaaga ggacttagaa gagtatgaaa 180
gtactctaag attttatcta agttgccttt tctgggtggg aaagtttaac cttagtgact 240
aaggacatca catatgaaga atgtttaagt tggaggtggc aacgtgaatt gcaaacaggg 300
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 360
gggtgccagcg caccagctag atgctctgtg acttctaggc cccattttcc cctctgaaaa 420
taagagggtt ggatcaaacg atctctgggg ccttagcatc tcaaactctg tggatcctcc 480
tacttacccc ttagagagcc ttactgggaa gtcagtcatt aatgatgtgg ccagttattt 540
gcaagtggta agagcctatt taccataaat aataactaaga accaactcaa gtcaaacctt 600
aatgccattg ttattgtgaa ttaggattaa gtagtaattt tcaaaattca cattaacttg 660
attttaaaaa cagttttgtg agtcatttac cacaagctaa atgtgtacac tatgataaaa 720
acaaccattg tattcctgtt tttctaaaca gtcctaattt ctaacactgt atatatcctt 780
cgacatcaat gaactttgtt ttcttttact ccagtaataa agtaggcaca gatctgtcca 840
caacaaactt gccctctcat gccttgctc tcaccatgct ctgctccagg tcagccccct 900
tttggcctgt ttgttttgtc aaaaaccta tctgcttctt gcttttcttg gtaatatata 960
tttagggaag atgttgcttt gccacacac gaagcaaagt aaataaagac cacaaatggt 1020
caaattctaa gccacttaat agcgttttgt acattaaaaa tgacaagggt tattatacaal 1080
gtagcctttt aaaaaattct cacacagaac agctttgtat ttagacttaa agctgttgct 1140
actttgctag tgacgtttgt gttaacagtc agtgctctag gccattgatt gattgattgt 1200
cagaatcaga agtgactaca caagagcatt agccagactt ttcagtgaga acaggtaaca 1260
ggctggcacc agcacttggt acagcacgtg gacaggacga cggaaccag agttctctgt 1320
ctctccttca cagcagatgg actcttctat aggtggctgt taatttacac aaagttatat 1380
tccagaatca ggaagccccg tgcgccaac acttgaagga gaactatgtt ccagttttgg 1440
tggtgaactt ctacgaaat acctactacc aaaaattgtg acaccttatt agacacttcc 1500
aaagtacccc ccaaaagctg tttaaaagac cattccattt tttcctacac aaagtgcata 1560
ctaaaatttc acaataatca tcttcagatg tacattttat ttagtacatt tcacagtttt 1620
cagtattcag tccctcatga acattttata gtcactctct cggccctgtt gtgaaatatg 1680
tgattccagt tcaattcaga gtgtatgatt ccgcttttca cgctgatcaa gtaaatattat 1740
gggtgtctct ttctgatctt caacattaaa aacatctatg tttctgtcat tccctgccag 1800
ggctgcttgc ttgtctgtct cagattctgc ttcattttca tccatgttgt agtcatctct 1860
tctctcagtt ttctgctggg ttctcccttc cccggcagct tctgtctcct cctcctgtcc 1920
gtcggggatg acaagctggg ctgctcagg gccctccatc tctggatttt cctggctcac 1980
tgacagggca gcctgcacct gtgggtctg gccagttct cgggctcccc cgaagcctct 2040
tccacctaca ggtctgtctt caacacctgc tcccggcctg gctcctgcgg cagcctgtcc 2100
ctctgagggt ccgatcaaca ctgatctcat ggttcccttc cca 2143

```

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## (2) INFORMATION ON SEQ ID NO. 83:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 450 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

tttttttaaa gccagctttt cttcagattt ttttggtggg caggctcgtga aagacaggtg 60
aggaagtaga tcttgggctc agcatgcctc taaaagtata atttcttttt tttaatgtgg120
aaagaaatgc ataactctgt ttctgttcct gtccccctct ctgcctctgt ggtgcctgag180
atactgggga tcccacagct ggggccactc agaggctacc aggaacgctt ccagtttgca240
tctggctgtt agtgccagga ccagaaaccc acagacctct tcacagacct cctgaccgtg300
atgtccctga agcctggaag gtgtccacac aatgaagcag aattgagtga tggggtgttt360
tgtggaaccc agtgaaactg tgtaacaca gtggaactgt gttaattttg agtggaagtt420
caagttccgt ggagttcatt gggcccgttt
450

```

## (2) INFORMATION ON SEQ ID NO. 84:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 408 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

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## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```

tgcaactgtg caccagctt gccagat tttt tccccattac acccccagtg tggcatatcc 60
ttgggtcccca gaggcacacc ccttgatctg tggacctcca ggcctggaca agaggctgct120
accagaaacc ccaggcccct gttactcaaa ttcacagcca gtgtggttgt gcctgactcc180
tcgccagccc ctggaaccac atccacctgg ggaggggcct tctgaatgga gttctgacac240
cgcagagggc aggccatgcc cttatccgca ctgccaggtg ctgtcggccc agcctggctc300
agaggaggaa ctcgaggagc tgtgtgaaca ggctgtgtga gatgttcagg gctagttcca360
accaagagtg tgctccagat gtgttggggc cctaacttgg cacagagt 408

```

## (2) INFORMATION ON SEQ ID NO. 85:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 311 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

tacagttttt atcagtgatc acatttttagt gtaatacatg aaactgagggc ttgatagaaa 60
acaggagaga aggcagtgagt gcatggggta catagggaga tgaggggcaag catcaccaag120
gagcggcagt gagatagacg ctctcatgga ctgctgcttt acaacctccc tggagagcaal80
tttaaaaata tgaatcaaga tcctttttgat ccactaatca tccagaaatc tacacagaaa240
tatgcacaaa aatatgtggg catccattga ctttccaacc tcttctcttt ccaggggggaa300
tattccttaa a 311

```

## (2) INFORMATION ON SEQ ID NO. 86:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 487 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```
gtcttttgaa atctgtttcc actacagcta tggcgaagtc tatcagccgg tgctaccagg 60
agtcactgcc agggctgccg ttctcctgaa cccagtggc cagaatcata agccctgacc120
ccatccctag aaagatgagg tcccagcaat ggccagagca tttctcacca gttctgtgag180
atagcacata aaaatagagt tctttgggca aaacttttgg gaagcaatgc atcctacatg240
ggctgatatt cagcctgagc tgttctcaag aggagagtgg tactggcagt ttatggctga300
aatccattct gattggttgg agtctatgct ataccagttg ttaaaccattt tgagtatcac360
tcttgcatac tgttactatt atatttcctc tatatataga cagaaaggcc attttttagga420
tattaaaggc tctgaaaatt tctgcagtag acccaactga aggttctatt aaggcagggt480
tcctaaa                                         487
```

(2) INFORMATION ON SEQ ID NO. 87:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1902 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```
gaggaaaaag aacaatgaac agcaacgatc ttgactgtgc aactcagaca ttctgcaga 60
aaagacatat gttgctttac aagaaggcca aagaactatg gggccttccc agcatttgac 120
tgttcattgc atagaatgaa ttaaatatcc agttacttga atgggtataa cgcataaatg 180
```

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```

tgtgatttta ttaggggcat ctgccaatc tctcactgtg gttccttctc tgactttgcc 240
tgttcatcat ctaaggaggc tagatccttc gctgacttca ccattcctca aacctgtaag 300
tttctcactt cttccaaatt ggctttggct ctttcttcaa cctttccatt caagagcaat 360
ctttgctaag gagtaagtga atgtgaagag taccactac aacaattcta cagataatta 420
gtggattgtg ttgtttgttg agagtgaagg tttcttggca tctgggtgct gattaaggct 480
tgagtattaa gttctcagca tatctctcta ttgtcttgac ttgagtttgc tgcattttct 540
atgtgctgtt cgtgacttgg agaacttaaa gtaatcgagc tatgccaact tggggtggtg 600
acagagtact tcccaccaca gtgttgaaag ggagagcaaa gtcttatgga taaaccctcc 660
tttcttttgg ggacacatgg ctctcacttg agaagctcac ctgtgctgaa tgtccacatg 720
gtcactaaac atgttatcct taaaccccc gtatgcctga gttgaaaggg ctctctctta 780
ttaggttttc atgggaacat gaggcagcaa atctattgct aagactttac caggctcaaa 840
tcatctgagg ctgatagata tttgacttgg taagacttaa gtaaggctct ggctcccagg 900
ggcataagca acagtttctt gaatgtgcca tctgagaagg gagaccagg ttgtgagttt 960
tcctttgaac acattggtct tttctcaaag ttctgacct gctagactgt tagctctttg1020
aggacagga ctatgtctta tcaatcacta ttattttcct gttacctagc atgggacaag1080
tacacaacac atatttgtgt agtcttctaa aagactcctc tgattgggag accatatctall140
taattgggat gtgaatcatt tcttcagtgg aataagagca caacggcaca accttcaagg1200
acatattatc tactatgaac attttactgt gagactcttt attttgcctt ctacttgcgc1260
tgaaatgaaa ccaaaacagg ccgttgggtt ccacaagtca atatatgttg gatgaggatt1320
ctgttgacct attgggaact gtgagactta tctggtatga gaagccagta ataaaccttt1380
gacctgtttt aaccaatgaa gattatgaat atgttaatat gatgtaaatt gctattttaag1440
tgtaaagcag ttctaagttt tagtatttgg gggattggtt tttattattt ttttctttt1500
tgaaaaatac tgagggatct tttgataaag ttagtaatgc atgttagatt ttagttttgc1560
aagcatgttg tttttcaa atatatcaagta tagaaaaagg taaaacagtt aagaaggaag1620
gcaattatat tattcttctg tagttaagca aacacttgtt gagtgcctgc tatgtgcacg1680
gcatgggccc atatgtgtga ggagcttgct taattatgta ggaagcaata gatctcggta1740
gttacgtatt gggcagatac ttactgtatg aatgaaagaa catcacagta atcacaatat1800
cagagctgag ttatccccag tgtagcttcg ttggggattc cagtttctg gaacgagagt1860
tagggccatt ttatttaaaa gaaactccc gttgagaccg gt 1902

```

(2) INFORMATION ON SEQ ID NO. 88:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1048 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

ctcacggtcg tctacacggt gttctacgcg ctgctcttcg tggtcatcta cgtgcagctc 60  
 tggctggtgc tgcgttacgg ccacaagcgg ctacagctacc agagcgtctt cctcttttctc 120

tgcctcttct gggcctcccg gcggaccgtc ctcttctcct tctacttcaa agaacttcgtg 180  
 gcggccaatt cgctcagccc ctctgtcttc tggtgtgctct actgcttccc tgtgtgcctg 240  
 cagtttttca cctcagcgt gatgaacttg tacttcacgc aggtgatttt caaagccaag 300  
 tcaaaatatt ctccagaatt actcaaatac cggttgcccc tctacctggc ctccctcttc 360  
 atcagccttg ttttctgtt ggtgaattta acctgtgctg tgctggtaaa gacgggaaat 420  
 tgggagagga aggttatcgt ctctgtgcga gtggccatta atgacacgct cttcgtgctg 480  
 tgtgccgtct ctctctccat ctgtctctac aaaatctcta agatgtcctt agccaacatt 540  
 tacttgagtg ccaagggctc ctccgtgtgt caagtgactg ccatcgggtg caccgtgata 600  
 ctgctttaca cctctcgggc ctgctacaac ctgttcaccc tgtcattttc tcagaacaag 660  
 agcgtccatt cctttgatta tgactggtac aatgtatcag accaggcaga tttgaagaat 720  
 cagctgggag atgctggata cgtattatct ggagtgggtg tatttggttg ggaactctta 780  
 cctaccacct tagtcgttta tttcttccga gttagaaatc ctacaaagga ccttaccacac 840  
 cctggaatgg tccccagcca tggattcagt cccagatctt tatttctttg acaaccctcg 900  
 aagatatgac agtgatgatg accttgccctg gaacattgcc cctcagggaac ttcagggaag 960  
 gttttgctcc agattactat gagttgggga caacaaacta acagcttcct ggcagaagca 1020  
 gggacttttg aaagcctcaa agtttgga 1048

## (2) INFORMATION ON SEQ ID NO. 89:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 804 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

gcccccatca gttcgaattt ctgcagtgag agcatctggg gttattgtga ccaactgaaa 60
gtctcagaga gtacccacgt gctccagccc ttctcccca gcateccttga tggcttaatt120
cacctagcag cccagttcag ctcaagggtc ctcaacctgg tgatggagac cctgtgcatc180
gtttgtacag tagaccccga attcacagca agcatggaaa gcaaaatctg ccccttcacc240
atcgccattt tcctaaagta cagtaatgat cccgtcgtcg cctcactggc tcaggacatc300
ttcaaggagc tgtcccagat tgaagcctgt cagggcccaa tgcaaataag gctgattccc360
actctgggtc gcataatgca ggccccagca gacaagattc ctgcaggggt ttgtgcgaca420
gccattgata tcctgacaac agtagtacga aatacaaagc ctcccctttc ccagcttctc480
atctgccaag ctttccctgc tgtggcacag tgtacccttc acacagatga caatgccacc540
atgcagaatg gcggagagtg cttgcgggcc tatgtgtcag tgaccctgga acaagtagcc600
cagtggtcatg atgagcaggg ccacaatgga ctgtggtatg tgatgcaagt ggtgagccag660
ctctgggacc cccgcacctc agagttcact gcggcctttg tgggcgcctt tgtttccacc720
ctcatctcca aggcagggcg ggaactcggg gagaatctag accagatttc ttcgtgccat780
ccttcagtta agatggcagg aggt                                     804

```

## (2) INFORMATION ON SEQ ID NO. 90:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 581 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

tctttgatca gatttagtgt cttaggtaat taaatcagaa agtctattta gctattctag 60
aagtgtatgt gtaggtattg ggtggttggg gttctttgag cgaacttgtc agaaactcca120
ttcttaacat cagaatcagg gcaggattga aaacattgtg gctggatctt gaaattgcta180
taacatctat tgcagaaaat gataggtcag atggatagca ataataatta tatatcagat240
cttagtaaca aaattaccaa gctttatcta gtggatatat gtaaaagaat atttttaaat300
gtccagcatt gatgtatttt ctttaagaat tattacagta tataagcatt ctttggaat360
acagtataaa aacataaatt ttttcgtatt tttaattttt tttatttttt tggccaagga420
tgaatcctcc cctgtaaaat attgattttc gcctaaattt cgggggtttcc ctggcacata480
atagcactgg ccccaacttc ggagatggcg gatgcgggta aaaagccaaa aggatggatg540
gggatccgga aatacgtggt ggaatggaag cgaatccaat a                                     581

```

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## (2) INFORMATION ON SEQ ID NO. 91:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2042 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

tggagatatt agtcagtttc tttagtata tttgtttcct tgatgtgcct ttttgttttt 60  
 ctttggggtt tttggaatcc ggatgctgtt gaagggcaat agcagactcc tccagctaag 120  
 agacaggaca tgttcttgag ccactgtagc tgttgaagct ggacaccaga cgctccctat 180  
 aacccccccg ccaggccata gcgtgtatgc atgtgcactt ccaccacacag aggaggggtg 240  
 gaagccttga gaacctcaag aaagggctgg attctgccat acctttgggt ctaccttggg 300  
 actgctgggt gccaacgtgt caaccagcct gtgttccttg ccaccacgc acttgctgag 360  
 gtgtggctga ggcagaatca tgtgaatggg tgcattcaag gagttcaggg cctgcttgg 420  
 agaagaaata ctttagcatc atgaaaggga aagaacgtgc acccctttt tgtttcttta 480  
 gtgaatgcaa gatttaataa aagtgaataa tgagcttccc ctttgggagt ggagcccagt 540  
 gcagctcact gacagggttg acatcagtat gatgtgttg actgaaactg tatgtctgta 600  
 ggtaggtgtg tgccttttag ggcagaccac ggtggccacc ccatttctcc aaggtgggtt 660  
 acctagcttg tgtatattag acattgccac cctcacctct ggccaaaaat tcttgattta 720  
 aaaagaaaag tctattttgt taacgacagg ctctgttgta tgtgttacta tcccaagcct 780  
 ggattatttt atttatttaa aagtatttta atttccatat tggctttatt ctaatcccat 840  
 ccatccctgt ggagctgcag agcatcttca tgtgagtaga cggatggaca taaatagatt 900  
 catgctcatt taggaagctg ggagtttctg gaagctgagg gtgagttcct gtgattcttg 960  
 ttcgcttcaa caaaaagtgg gagaccaagt ttttatagca aaagaccaa ttagctgtag 1020  
 agtcttgaat gcagaaaaaa attaccctag ctttcttagc acttaggggt ttgtgaggat 1080  
 tcagtgttta gcacagtgtc tggcacatag taagccctag taaatgttaa atattgttat 1140  
 tagtgtttcg taaaacttga gaaatagagc tgagctcatt cccttcctgt tgattcaaaa 1200  
 ataataccta catgaaaaca tgattccaag ttgattgaat gttgtaggaa ttactgggtt 1260  
 agagtagccc agttctcggc ctaccctgct ggttgggata ttactgtatt cttgaatgca 1320  
 ctggtttgaa aatatgccag acttcagccc ccaaggaaac aaggctgcaa gaatttatga 1380  
 actccagctg gaaaaggtaa aggtgacctt tggctagcca catactggac cttaccccacl 1440  
 tgacgtcttt cagaacattc caagggtttt cctcaaggaa catttttgag ctagaaatta 1500  
 aaatgggttc tctggcagac tgcaccctt gagtcaaaagt taacagtatt cctttgaatg 1560  
 caataataga ggcttttctg cgtaaggga gaaggaatga ccaattgaac ttacacattc 1620  
 cccaggcagg tccctttgcc ggccctaca ggctgggggtg gccctcctg tcctcaggga 1680  
 tcagactccc agactggtta gttctgcatg tttccatcaa attaaagggt attccctggc 1740  
 cgctcctgg agaaaaccaa cccacccctg ccagctgggg gcaatggggc agggattttg 1800  
 gcctctcaga acagctccta gaggtgctc atgactgaat gttttccaa atcacctaa 1860  
 tatcggtttg ctttttgttt tgggggagag gatttagcct cttacttccc tgatggattc 1920  
 aaagttttat ctatctcctt atctcctgcc ctgtcttggc acaactctgg atagattgca 1980  
 ggtgtggaat ttgctggagt ttggtggctc cccaaattcc ttgatctgtc cgcaaagaga 2040  
 ag

2042

09673395.12200

## (2) INFORMATION ON SEQ ID NO. 92:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 430 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

gttaaaaacc tagtattcat tttttttttt cctgtaccaa aacaatcatc ttccttttatt 60
tttcctggag cggaagagg agagtggaga agaagggag aatgcaaagt gtcactttga120
acttctcggt caccacacac gtgggagtc actcatgtca gcagcctccg tgcacaggcc180
ccagggtgaaa gaaagaatga ggtctagttg gaccagctaa cactgcctgc cttgtgttta240
cgaaaggcag ctgcctctgt ggtgtgattt caggggagcc agacagggcc ggggccacga300
acctgcatcc tgcctcctaa gcacctattt gccatgcggt gaggcttaac ttgggaaact360
tcaatttgct tggggtgcag attagctttc caaactattg tgatgctcat gcttgacttc420
ccaaggactt                                     430

```

## (2) INFORMATION ON SEQ ID NO. 93:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 592 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

09673395 122700

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```
aattaaaata aatagaaaca tacggagatt cttttatggt ggatttatta taccctccac 60
catttttggt cctgaaaagg gaaaagatac acggtcagat agtacaggta tgtgtttcccl120
actacacatt atggctataa tggagttgaa ttgcaaacag taaaattttg ttttggttg180
gtttcccttg atccccccag acaggagctt cctctcccac cctacctgcc tgcccttaag240
ttgtgtccta ttaaactgga cacaaatctc accggctttt agtctaataa ttgaatcata300
gctacacacg gtgacaccag aatagctact tgttttttta tgttaccagt gagtaacttg360
tttatccttg tatgtagaaa ctaatttcac catgatcaca gatctgtgta acatctctag420
tttgaatttc cacacaattt taaaatgtct actaggaaaa cttacacctt tttgttccaa480
gggtgctctt catctattaa aaccgtgggg gcatacttcc agtgttgctt ctgagggcca540
aattttgtgg gtcgtggggg acaattttgt attaacatac gttattttgt aa 592
```

(2) INFORMATION ON SEQ ID NO. 94:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 674 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```
aaggccgcgc aagtgcactt gcgtgtcacc gttaccgtag cgactgggct tctggactgt 60
atatacctagc tgccttggtca acatcttcga gcacggcagc ctccggaggc cggggtaact120
ggcagcaggt aggaaactat gtgaaagaat ctctgatgt cataatttcc ggggtgcacc180
ggaacatttg atcatcattc ctttggaat tccagccttc tgtggaaaag ccagtagaaa240
gcattgattt attcacctct acaggaatca gactcagcct cttttgggtt tcagtgaagt300
atgccttttc aatttggaac ccagccaagg aggtttccag tggaaggagg agattcttca360
attgagctgg aacctgggct gagctccagt gctgcctgta atgggaagga gatgtcacca420
accaggcaac tccggagggt ccctggaagt cattgcctga caataactga tgttcccgtc480
actgtttatg caacaacgag aaagccacct gcacaaagca gcaaggaaat gcatacctaaa540
tagcaccatt aagtcttttg tcaaggctct actaggtcaa gggtaatgga ccagtatcat600
ctgggtgatct ggtaaacaaa taaaagtggg ggcaccttta gatgatgaaa aaaaaaaaaa660
aaaaaaaaaa aaaa 674
```

004227 5652960

## (2) INFORMATION ON SEQ ID NO. 95:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 324 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```
gttccttttca ttccatcact ttaggtgatg ggtaagattt ttgaaagcct tatatTTTTT 60
gattttgttg tctagtttaa tctaccttt aatagtttg tttggtaaaa ttcccacttg120
aatgtgacac tgataataat tatgctgatt ttttagcatct cttataggaa tcaaagttta180
ttaaagttac atagaggatt gaaaaatgta taccactcaa tttttatcta aggagggata240
gggtataaag ggaggtacct aaatagctca aataatggat ataatccttt tttccataac300
catttgggat gctttaaggc aatt                                     324
```

## (2) INFORMATION ON SEQ ID NO. 96:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 709 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

ggatgcgcca ctataacatc cccgtcagag tgtgtgagga gaccagtcta tgagagacgc 60
atgctcctga cagcctggcg acgtggcgaa gatgcacagg tggctcctgg gcttgggctg120
caggtttggg ggtctctaag aacaatctct gagaagaacc cttggggccc tgggagccaal80
gttggacagg atgtcctgaa gactagcttt tgataagaga aattaaccaa gtctttcccc240
tcctctatga tgcaatatat ttcagtgggg gccttcagag cacacctgtt ggacggtgca300
aaccatatct tctccagaag gcaaataact ttgtatcaga ggaaactcag ttttggagag360
gaatatgttc tttatatctc aaatcaaaac tctctctaag ggtaaactgg cttctaattt420
ttttaagtac agtatTTTTT tttccccttt agtagtaacg ggtttctata gatcttccta480
tacagtctgc tttaaactcag gaccttgaga ttatgagact gacgtgctgc ccactgcact540
gagggggctt ctaacagtct gctttaagtg gtataattct gggatagatc tggtactggc600
atagtcatga caacctctgg taatcttacc ttctcctttt tatgaaggga agagcaatgg660
tttggaacta catctaaatt aaggctatTT taagcagatt gttttgcaa 709

```

## (2) INFORMATION ON SEQ ID NO. 97:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 562 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```

gtccagatgg aatgactccc atcctctcct catctcccct ttgacgagcc tcaaactgct 60
cagctcatca aagagccatt gccaaacttc gtatgtggtt ctgggtccca gggagccttg120
gaacctggca ccctgggggtg gtttaattcc ggcacgagag cattcctgct tctcaaggga180
cacagtggcc tgcattggggc agcatggacc ctgggctgat catgtgcatt cctgcttctc240
tggggacaca gtggggccac atggggccagc atggaccctg ggctagagca agcacatctc300
catctcttcc acctcaggca gtgtggctcc agatgtcagg agggactgac ctgaggacct360
tccaggttcc tctgtgcccag gaatgagagg ccaggcccga tcctaccacc tcgccttgac420
cctgaagtca gagcaggcca gccaaagcagg aagcacactg ttttaatttt tgcatggaaa480
gtaaatgtgt actttgatag ggtaaaaata tggctctttt taagttgctc aaccccataa540
tttgagccat tgccttgctt aa 562

```

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 98:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1948 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

gatcaccaag acacacaaaag tagaccttgg gctcccagag aagaaaaaga agaagaaagt 60
ggtcaaagaa ccagagactc gatactcagt tttaaacaat gatgattact ttgctgatgt 120
ttctccttta agagctacat cccctctaa gagtgtggcc catgggcagg cacctgagat 180
gcctctagtg aagaaaaaga agaagaaaaa gaagggtgtc agcacccttt gcgaggagca 240
tgtagaacct gagaccacgc tgcctgctag acggacagag aagtcaccca gcctcaggaa 300
gcagggtgtt ggccacttgg agttcctcag tggggaaaaa aaaaataaga agtcacctct 360
agccatgtcc catgcctctg gggtgaaaac ctcccagac cctagacagg gtgaggagga 420
aaccagagtt ggcaagaagc tcaaaaaaca caagaaggaa aaaaaggggg cccaggaccc 480
cacagccttc tgggtccagg acccttggtt ctgtgaggcc agggaggcca gggatgttgg 540
ggacacttgc tcagtgggga agaaggatga ggaacaggca gccttggggc agaaacggaa 600
gcggaagagc cccagagaac acaatgggaa ggtgaagaag aaaaaaaaaa tccaccagga 660
gggagatgcc ctcccaggcc actccaagcc ctccagggtc atggagagca gccctaggaa 720
aggaagtaaa aagaagccag tcaaaagtga ggctccggaa tacatcccca taagtgatga 780
ccctaaggcc tccgcaaaaga aaaagatgaa gtccaaaaaag aaggtagagc agccagtcac 840
cgaggagcca gctctgaaaa ggaagaaaaa gaaggagaga gagagtgggg tagcaggaga 900
cccttggaag gaggaacacg acacggactt agaggtgggt ttggaaaaaa aaggcaacat 960
ggatgaggcg cacatagacc aggtgaggcg aaaggccttg caagaagaga tcgatcgca 1020
gtcaggcaaa acggaagctt ctgaaaccag gaagtggacg ggaaccagc ttggccagt 1080
ggatactgct ggttttgaga acgaggacca aaaactgaaa tttctcagac ttatgggtgg 1140
cttcaaaaaa ctgtcccctt cgttcagccg ccccgccagc acgattgcaa ggcccaacat 1200
ggccctcggc aagaaggcgg ctgacagcct gcagcagaat ctgcagcggg actacgaccg 1260
ggccatgagc tggaaagtaca gccggggagc cggcctcggc ttctccaccg ccccaacaal 1320
gatcttttac attgacagga acgcttccaa gtcagtcaag ctggaagatt aaactctaga 1380
gttttgtecc cccaaaactg ccacaattgc tttgattatt ccatttatgc tggagattac 1440
aaattttttt tgtgaaaaaa tcagatcttg gtgaggacct cgagcagtaa gatataaata 1500
actcccataa gcttagcggt ccagtaatgg aacactaggc ataatgggtt tattcagttg 1560
tgcaaatgaa agccatctga cagttggctc acattgaaca cctgtggaga ttaaggacga 1620
ggacaactat attgatgggc ttggatgaac tggggcaggg cagctcatat ttccgggagc 1680
aggagaacga gtgagtgtca aaacctcctg tttctgtgt taaacattcc gtccctgttt 1740
gagacatcag tatgtacagt taacttttgc tgagtgttta gcaggtaacta gggacatact 1800
agtgttttcc ttaattgtatt taatcttcat aattatgaaa tgggtgctat tattagcccc 1860
atcttataga tgaggcaact gaggttcagg gataaagtaa taaaattgcc tggggtcacc 1920
cagccactaa aaaaaaaaaa aaaaaaaaaa

```

1948

00673395-122700

## (2) INFORMATION ON SEQ ID NO. 99:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 483 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

aatttatggg gtctatcttt gaccacgtga taccacttac ctgattctat gtactgatta 60
atgtatctaa cagttttata gtgaaagtac tttttaaaaa agtatttgaa tgggtcatttc120
tatttttccc cctttgctgt acaagttaat ttttactcat cttttgctgt acaaattaac180
tttcatcaat acaaataaga ggctagtttt aagtcaattt atttgtcatg agcccaggaa240
caattaaatt ctataaagta atgtattaaa atagtacact ttaaaaaatta ttttccttct300
ttttttctct ttaaatttta agaccatcat aataaattat cattacaaag tcaaacatac360
tatatactac tatcagtcaa tggggaaaaa ataagtccat atgttttatg ggtaaaatgc420
tgtaatagat tgggattgtc caatttgcct tgaaaaaaat cacagcagtt tttaggtttc480
cct

```

483

## (2) INFORMATION ON SEQ ID NO. 100:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 437 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

004221"56E2960



## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

cccgcttgag gcgtaggggg tggcgctctc cgctcggcgg cgctcccatg gcgcacatta 60
ccattaacca gtacctgcag caggtgtacg aagccatcga cagcagagat ggagcatctt120
gtgcagagtt ggtgtctttt aaacatcctc atgttgcaaa cccacgactt caaatggcct180
ctccagagga gaagtgtcaa caagtcttgg aacccoctta tgatgaaatg tttgcagctc240
atttaagggtg cacttatgca gtggggaatc atgaattcat agaggcatac aagtgccaga300
ccgtgatagt ccaatcattc ttgcgagcat tccaggccca caaagaagaa aactgggctc360
tgctgtcatg tatgcagtag cgcttgacct ttcgagtgtt tgccaataat gcagttcaac420
cagttgggta aggaagg

```

437

## (2) INFORMATION ON SEQ ID NO. 101:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 359 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

cagatctagg ggcttcagct gtgtgcagac cccatgccac ttcagggag tgacacaggc 60
ctgtgtcatc tcgctttggc agcaggtggg tggccttcct caggggagga ggtggcctga120
gatgtgtttc aggtctttga cccatcactc cctacacaca cgacgtgaac accactcctg180
gagcattctc agaatggaga tttgaattcc atgtggcagc ttctcacaca caaacctgcc240
atcattcccc acacacccac tcacgacatt caacagccat gagccaaaag aagttccttg300
tttcagattt gaagggttta tgaatccact tcttcggat gtagctcttt aatgatattt 359

```

## (2) INFORMATION ON SEQ ID NO. 102:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 501 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual

002227-5622960

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```
tccggcgtcac atcctgagtc ggcctctctgc cgaggcggag cggacatgca ggctccccgc 60
ggcaccctag tcttcgccct ggtgatcgcg ctctgtcccg tcggccggga accttctagc120
caaggatctc agagtgtctt acagacatat gagctgggaa gtgaaaacgt gaaagtccct180
atctttgagg aagatacacc ctctgttatg gaaattgaaa tggaagagct tgataaatgg240
atgaacagca tgaatagaaa tgccgacttt gaatgtttac ctaccttgaa ggaagagaag300
gaatcaaata acaaccacaag tgacagttaa tcctaaacct gaatggcgct catgttttcc360
aagagaagca gccctgaggg gagtctgctg aggctgcaa cagaggatga agaggataca420
aatttaatta atttcaaata aacatagaca caagaacctt ttgctgtttc ttccaacgcc480
cactcttcct aatgatggca t                                     501
```

(2) INFORMATION ON SEQ ID NO. 103:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1102 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00/22/95 12:27:00

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

cgggatctcc cgaaggaatt tacggggatt cctcggacca ttatcctcag gcaagaaaca 60
aaaccaaact tggactctcg tgcagaaaat gtagccatt accacatgta gccttggaga 120
cccaggcaag gacaagtaca cgtgtactca cagagggaga gaaagatgtg taaaaaggat 180
atgtataaat attctattta gtcacctcga tatgaggagc cagtgttgca tgatgaaaag 240
atggtatgat tctacatag taccattgt cttgctgttt ttgtactttc ttttcaggtc 300
atttacaatt gggagatttc agaaacattc ctttcaccat catttagaaa tggtttgctt 360
taatggagac aatagcagat cctgtagtat ttccagtaga catggccttt taatctaagg 420
gcttaagact gattagtctt agcatttact gtagttggag gatggagatg ctatgatgga 480
agcataccca ggggtggcctt tagcacagta tcagtaccat ttatttgtct gccgctttta 540
aaaaataccc attggctatg ccacttgaaa acaatttgag aagttttttt gaagtttttc 600
tcaactaaaat atggggcaat tgtagcctt acatgttgtg tagacttact ttaagtttgc 660
acccttgaaa tgtgtcatat caatttctgg attcataata gcaagattag caaaggataa 720
atgccgaagt cacttcattc tggacacagt tggatcaata ctgattaagt agaaaatcca 780
agctttgctt gagaactttt gtaacgtgga gagtaaaaag tatcggtttt attctttgct 840
gatgtccttt ctgcttgaaa taacagtcac catacagcta aaggagagga gtttctttcc 900
ttctaagtag gcagaaatgg tatcattatg ttgccgtctt ccaatctccc agagctcgtt 960
ctctagagaa tcaccttctt tcgcgttttt tttttttttt gagggtagga gtctcactat 1020
gttgcccaa gactaggcct gggaactgtt ggggggcaa ggggattgct ccggtcccgc 1080
aggctcccc agtaggccg ga

```

1102

## (2) INFORMATION ON SEQ ID NO. 104:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 306 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

gaccaacctt ccttgccatt tatacggcat aaaacctca atctcaccag tatggctacc 60
aaaattatag gttcacctga aacaaagtgg attgatgcaa cttctggaat ttacaactca 120
gaaaaatctt caaatctatc tgtaacaact gatttctcgg aaagccttca gagttctaatt 180
attgaatcca aagaaatcaa tggaattcat gatgaaagca atgcttttga atcaaaagca 240
tcttgaatcc attttttttg aaaaacctta aaaagggcga tcacaatttt tttgaacaag 300
ggtcat

```

306

00221-5552950

## (2) INFORMATION ON SEQ ID NO. 105:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2042 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

tggagatatt agtcagtttc tttagtgata tttgtttcct tgatgtgcct ttttgttttt 60
cttttggggtt tttggaatcc ggatgctggt gaagggaat agcagactcc tccagctaag 120
agacaggaca tgttcttgag ccactgtagc tgttgaagct ggacaccaga cgctccctat 180
aaccoccccg ccaggccata gcgtgtatgc atgtgcactt ccaccacag aggaggggtg 240
gaagccttga gaacctcaag aaagggtggt attctgccat acctttgggt ctaccttggg 300
actgctgggt gccaacgtgt caaccagcct gtgttccctg ccaccacgc acttgctgag 360
gtgtggctga ggcagaatca tgtgaatggg tgcattcaag gagttcaggg ccctgcttgg 420
agaagaaata cttagcatc atgaaaggga aagaacgtgc accccttttt tgtttcttta 480
gtgaatgcaa gatttaataa aagtgaataa tgagcttccc ctttgggagt ggagcccagt 540
gcagctcact gacagggttg acatcagtat gatgtgttgg actgaaactg tatgtctgta 600
ggtaggtgtg tgccttttag ggcagaccac ggtggccacc ccatttctcc aagggtggtt 660
acctagcttg tgtatattag acattgccac cctcacctct ggccaaaaat tcttgattta 720
aaaagaaaaa tctattttgt taacgacagg ctctgttcta tgtgttacta tcccagcct 780
ggattatttt atttatttaa aagtatttta atttccatat tggctttatt ctaatcccat 840
ccatccctgt ggagctgcag agcatcttca tgtgagtaga cggatggaca taaatagatt 900
catgctcatt taggaagctg ggagtttctg gaagctgagg gtgagttcct gtgattcttg 960
ttcgcttcaa caaaaagtgg gagaccaagt ttttatagca aaagaccaa ttagctgtag 1020
agtcttgaat gcagaaaaaa attaccctag ctttcttagt atttaagggt ttgtgaggat 1080
tcagtgttta gcacagtgtc tggcacatag taagccc... attttaa atattgttat 1140
tagtgtttcg taaaacttga gaaatagagc tgagctcatt ctgt tgattcaaaa 1200
ataataccta catgaaaaca tgattccaag ttgattgaat gttgtaggaa ttactggttt 1260
agagtagccc agttctcggc ctaccctgct ggttgggatc ttactgtatt cttgaatgca 1320
ctggtttgaa aatatgccag acttcagccc ccaaggaaac aaggctgcaa gaatttatga 1380
actccagctg gaaaaggtaa aggtgacctt tggctagcca catactggac cttacccac 1440
tgacgtcttt cagaacattc caagggtttt cctcaaggaa catttttgag ctagaaattal 1500
aaatgggttc tctggcagac tgcacccctt gagtcaaagt taacagtatt cctttgaatg 1560
caataataga ggcttttctg cgttaaggga gaaggaatga ccaattgaac ttacacattc 1620
cccaggcagg tccctttgcc ggcccctaca ggctggggtg gcccctcctg tcctcaggga 1680
tcagactccc agactggtta gttctgcatg tttccatcaa attaaagggt attccctggc 1740
cgctccttg agaaaaccaa cccacacctg ccagctgggg gcaatggggc agggattttg 1800
gcctctcaga acagctccta gaggtgctc atgactgaat gttttcccaa atcacctaaa 1860
tatcggtttg ctttttgggt tgggggagag gatttagcct cttacttccc tgatggattc 1920
aaagttttat ctatctcctt atctcctgcc ctgtcttggc acaactctgg atagattgca 1980
ggtgtggaat ttgctggagt ttggtggctc cccaaattcc ttgatctgtc cgcaaagaga 2040
ag

```

2042

09673395-12700

## (2) INFORMATION ON SEQ ID NO. 106:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 320 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```
aatcttttta ccatgaaatt tcttccagaa ttttccccct ttgacacaaa ttccatgcat 60
gtttcaacct tcgagactca gccaaatgtc atttctgtaa aatcttccct gagtcttcca120
agcagtaatt tgccttctcc tagagtttac ctgccatttt gtgcacattt gagttacagt180
agcatgttat ttacaattg tgactctcct gggagtctgg gagccatata aagtgggtcaa240
tagtgtttgc tgccttgaga gttgaatgac attttctctc tgttttggta ttactgtaga300
tttcgatcat tctttggtta                               320
```

## (2) INFORMATION ON SEQ ID NO. 107:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 506 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00673395.12200

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

gtcgaacagc aaagccaaga cttgttaaaa aggtttgaag aggaaggacc ataacaattg 60
aaagggggaa attataagat acagtaaatt cctcttcaaa gatttagcct gttgacttcc120
ttattccttg ttctcaaact cgacttcctt gttgtccatg cctccttgtc cctagttact180
gtgaacaacc ttcccaccag ttctaataca taactcacat ctgctccctt gggtaccac240
tctgcaccca ttcttccac tgaaactgca cttcccacca ctgtaactca catccccctt300
cccttcctta tttggaaaag tattcacaaa tagccaatcg ggtcaactta gaatgagcgg360
tccaacccca gcccctgggg gagtgacaca gaggtaggga ctgtgttagg gataaaaacc420
ttttcctttc tttgttcagt gtgctgctgt gatcatgatt gatgcaggca gcagcctttt480
tgcagaagta aattgccttg ctgagg                                     506

```

## (2) INFORMATION ON SEQ ID NO. 108:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1276 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00422T 56557960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

gcgcgccggg cgccctgcggg gcgagagggg cggggcggaag gggaagctac gtcccggagg 60
tgcggtgtgg ggcaccgggc ggggcccggg gaaccggcgc cccacggagc tgctgctgtc 120
agaccaaccc cgggccccca tcatcactgc gccgcgcttt caggcgccga gaactaccgt 180
tcccggcatg ccatgaaatt ggcctcggcg ctgaggcggg gtccggccct ccaccgcgtc 240
ccgcccgcgc cgaatcgcgg tcgcgagcca tggaggagga ggcacgtcc ccggggctgg 300
gctgcagcaa gccgcacctg gagaagctga ccctgggcat cacgcgcac ctagaatctt 360
ccccagggtg gactgagggt accatcatag aaaagcctcc tgctgaacgt catatgattt 420
cttcctggga acaaaagaat aactgtgtga tgcctgaaga tgtgaagaac ttttacctga 480
tgaccaatgg cttccacatg acatggagtg tgaagctgga tgagcacatc attccactgg 540
gaagcatggc aattaacagc atctcaaaac tgactcagct caccagctc tccatgtatt 600
gacttcctaa tgcacccact ctggcagacc tggaggacga tacacatgaa gccagtgatg 660
atcagccaga gaagcctcac tttgactctc gcagtgtgat atttgagctg gattcatgca 720
atggcagtg gaaagtgtgc cttgtctaca aaagtgggaa accagatta gcagaagaca 780
ctgagatctg gttcctggac agagcggtat actggcattt tctcacagac acctttactg 840
cctattaccg cctgctcacc acccactctg gcctgcccc gtggcaatat gccttcacca 900
gctatggcat tagccacag gccaaagcaat ggttcagcat gtataaacct atcacctaca 960
acacaaacct gctcacagaa gagaccgact cctttgtgaa taagctagat cccagcaaag1020
tgtttaagag caagaacaag atcgtaatcc caaaaaagaa agggcctgtg cagcctgcag1080
gtggccagaa agggccctca ggaccctccg gtccctccac ttcctccact tctaaatcct1140
cctctggctc tggggaaacc ccaccggga agttgaggca cccttccttc caatttgct1200
aaccagtttc caggagtggg gtgggtttt ccgtggcaca ggttggggcc ttaggggggg1260
ttggacgttc catttt 1276

```

## (2) INFORMATION ON SEQ ID NO. 109:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 373 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```

aaatacattt atgtttcttg aaatgtgtta agtggccttt gtcaagggtg ttataataga 60
agagtatata aaaatgaatt tctctagaga tgcagcatat tctaaagatc catcattaga120
taattaaaaa tatgtaagtc atgctaacat ttccatatat aaatggagaa cattaactct180
cctactgttt agttataaaa taccaaaatt tgtaattatc ctatctggaa ttacactata240
ctgcaaaaat gccagttact tcaactttta atttgacaat gtatgtgatg aattataaaa300
tttaatagcc tacatctttt cctccttgta tccaaaattt tccggacctt aatgcttaaa360
ccttttggtt acc 373

```

## (2) INFORMATION ON SEQ ID NO. 110:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 492 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

gtcttttgaa atctgtttcc actacagcta tgggtcaagtc tatcagccgg tgctaccagg 60
agtcactgcc agggctgccg ttctcctgaa cccagtggc cagaatcata agccctgacc120
ccatccctag aaagatgagg tcccagcaat ggccagagca tttctcacca gttctgtgag180
atagcacata aaaatagagt tctttgggca aaacttttgg gaagcaatgc atcctacatg240
ggctgatatt cagcctgagc tgttctcaag aggagagtgg tactggcagt ttatggctga300
aatccattct gattggtttg agtctatgct ataccagttg ttaaacattt tgagtatcac360
tcttgcatatc tgttactatt atatttcctc tatatataga cagaaaggcc attttaggaa420
tatttaaagg gctcttgaaa attttctggc attagaccca actgaagggt ctattaaggc480
agggttccta aa

```

## (2) INFORMATION ON SEQ ID NO. 111:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1678 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

09673395.123700



(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

gcctcagcag actccttggg cggtagcagg gagatggtgc aacggcccca gcctgcacag 60
gaaccgagca ggcctggatc tgccaacccat agacacggga tatgattccc agccccagga 120
tgtcctgggc atcaggcagc tggaaaggcc cctgcccctc acctccgtgt gttacccccca 180
ggacctcccc agacctctca ggtccaggga gttccctcag tttgaacctc agaggtatcc 240
agcatgtgca cagatgctgc ctcccaatct ttccccacat gctccatgga actatcatta 300
ccattgtcct ggaagtcccg atcaccagggt gccatatggc catgactacc ctcgagcagc 360
ctaccagcaa gtgatccagc cggctctgcc tgggcagccc ctgcctggag ccagtgtgag 420
agggcctgac cctgtgcaga aggttatcct gaattatccc agcccctggg accaagaaga 480
gaggcccgca cagagagact gtccttttcc ggggcttcca aggcaccagg accagccaca 540
tcaccagcca cctaatagag ctggtgctcc tggggagtcc ttggagtgcc ctgcagagct 600
gagaccacag gttccccagc ctccgtcccc agctgctgtg cctagacccc ctagcaaccc 660
tcagccaga ggaactctaa aaacaagcaa ttgcccagaa gaattgcgga aagtctttat 720
cacttattcg atggacacag ctatggagggt ggtgaaattc gtgaactttt tggttggtaaa 780
tggcttccaa actgcaattg acatatttga ggatagaatc cgaggcattg atatcattaa 840
atggatggag cgctacctta gggataagac cgtgatgata atcgtagcaa tcagccccaa 900
atacaaacag gacgtggaag gcgctgagtc gcagctggac gaggatgagc atggccttaca 960
tactaagtac attcatcgaa tgatgcagat tgagttcata aaacaaggaa gcatgaattt1020
cagattcatc cctgtgctct tcccaaatgc taagaaggag catgtgccc cctggcttcal1080
gaacactcat gtctacagct ggcccaagaa taaaaaaaac atcctgctgc ggctgctgag1140
agaggaagag tatgtggctc ctccacgggg gcctctgccc acccttcagg tggttccctt1200
gtgacaccgt tcatccccag atcactgagg ccaggccatg tttggggcct tggttctgacal1260
gcattctggc tgaggctggg cggtagcaact cctggctggg ttttttctgt tcctccccgal1320
gaagccctct ggccccaggg aaacctgttg tgcagagctc ttccccggag acctccacac1380
accctggctt tgaagtggag tctgtgactg ctctgcattc tctgctttta aaaaaaccat1440
tgcaggtgcc agtgtcccat atgttccctc tgacagtttg atgtgtccat tctgggcctc1500
tcagtgttta gcaagtagat aatgtaaggg atgtggcagc aaatggaaat gactacaaac1560
actctcctat caatcacttc aggtacttt tatgagttag ccagatgctt gtgtatcctc1620
agaccaaaact gattcatgta caaataataa aatgtttact cttttgtaaa aaaaaaaa 1678

```

002227"56552950

## (2) INFORMATION ON SEQ ID NO. 112:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 866 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

gtcgccatga ctgccaagga ctgctccatc atgattgcac tgtctccctg tctgcaggat 60
gccagctctg atcaaaggcc tgtggtccct tcatcgaggt ccaggtttgc cttttccgtg120
tctgtgctgg accttgacct caagccctac gagagcattc cccatcagta taaactggac180
ggcaagatcg tcaactatta ttcaaagact gtacgtgcca aagacaacgc cgtgatgtcg240
actcggttca aggaaagcga agattgcaca ttagttctcc acaagggtcta actctttccc300
tgcagtgtct ttgaaacttg aacataatgt gaaggctgaa tgatagagat attttctgtt360
gtgttgggtg accttttggt gtgaatgttt ttgcttttaa ccccttttga ggtgggattg420
cctcttgag acatggaatt gaagagcact agaaacaact tcctggacaa ggaatgtagg480
aagtgaagtgc tgtgtcccag gaagctgctc acactcttaa aatggaagtg tccgttaagc540
cctgggaaga cgttctggat agttcttctt tcccaaccag ggctcatgtc tgattctcta600
atgcgaaaag ccttattcta agaccaagg tttggatctg ctaccaccag actcctaaca660
tagaaaactt gaattgtcac atacatttta cagtttgac ttttaagaaa acatggatac720
tactgggaac ttccccccagc tgagttacat gggcactttt tcagtgcagg ccacatatca780
acacagggtt ttaaggtggg tgcttggtg cacacgtgaa ccccggtggc cccagatgc840
cgattctgag ccagtgtaga cccagg
866

```

## (2) INFORMATION ON SEQ ID NO. 113:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

09673395 122700

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

gcgcggccgg cgctgcggg gcgagagggt cggggcggaag gggaagctac gtcccggagg 60
tgcggtgtgg ggcaccgggc ggggccgcgg gaaccggcgc cccacggagc tgctgctgtc 120
agaccaaccc cgggccccca tcatcactgc gccgcgcttt caggcgccga gaactaccgt 180
tcccggcatg ccatgaaatt ggccctcgcg ctgaggcggg gtccggccct ccaccgctc 240
ccgcgcgcgg cgaatcgcgg tcgcgagcca tggaggagga ggcacgtcc ccggggctgg 300
gctgcagcaa gccgcacctg gagaagctga ccctgggcac cagcgccatc ctagaatctt 360
ccccagggtg gactgagggtg accatcatag aaaagcctcc tgctgaacgt catatgattt 420
cttcctggga acaaaagaat aactgtgtga tgctgaaga tgtgaagaac ttttacctga 480
tgaccaatgg cttccacatg acatggagtg tgaagctgga tgagcacatc attccactgg 540
gaagcatggc aattaacagc atctcaaaac tgactcagct caccagctc tccatgtatt 600
cacrtccctaa tgcacccact ctggcagacc tngaggacga tacacatgaa gccagtgtatg 660
atcagccaga gaagcctcac tttgactctc gcagtgtgat atttgagctg gattcatgca 720
atggcagtgg gaaagtttgc cttgtctaca aaagtgggaa accagcatta gcagaagaca 780
ctgagatctg gttcctggac agagcggtat actggcattt tctcacagac acctttactg 840
cctattaccg cctgctcatc acccacctgg gcctgcccc gtggcaatat gccttcacca 900
gctatggcat tagccacag gccaaagcaat ggttcagcat gtataaacct atcacctaca 960
acacaaacct gctcacagaa gagaccgact cttttgtgaa taagctagat cccagcaaag1020
tgtttaagag caagaacaag atcgtaatcc caaaaaagaa agggcctgtg cagcctgcag1080
gtggccagaa agggccctca ggaccctccg gtccctccac ttctccact tctaaatcct1140
cctctggctc tggaaacccc acccggaagt gagcacccct ccctccaaact ccctaccagc1200
tccagagtgg tggtttccat gcacagatgg ccctaggggt gacctccagt tttgcgtgtg1260
gaccgtaggc ctctttctag ttgaatgacc aaaattgtaa ggcttttagt cccaccgacal320
ttagccaggc tcgtagtgag gcctccagag caggttgtgc tgtcccctgc ctctggaagc1380
aatggggaat gtggaatcaa gacaatgcc aaaaaatttt taatgcagct ggtc 1434

```

(2) INFORMATION ON SEQ ID NO. 114:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 914 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

002227 5622360

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```

ttggcagcgg ggagagggaa agaggaggaa atgggggttg aggaccatgg cttacctttc 60
ctgcctttga cccatcacac cccatttcct cctctttccc tctccccgct gccaaaaaaa120
aaaaaaaaag aaacgtttat catgaatcaa cagggtttca gtccttatca aagagagatg180
tggaagagagc taaagaaacc accctttgtt cccaactcca ctttaccatc attttatgca240
acacaaacac tgtccttttg ggtccctttc ttacagatgg acctcttgag aagaattatc300
gtattccacg tttttagccc tcagggttacc aagataaata tatgtatata taacctttat360
tattgctata tctttgtgga taatacatc aggtggtgct gggtgattta ttataatctg420
aacctaggtat tatccttttg tcttccacag tcatgttgag gtgggctccc tggatggta480
aaaagccagg tataatgtaa cttcacccca gcctttgtac taagctcttg atagtggata540
tactctttta agtttagccc caatataggg taatggaaat ttcctgccct ctgggttccc600
catttttact attaagaaga ccagtataaa tttaataatg ccaccaactc tggcttagtt660
aagtgaagag gtgaactgtg tggcaagaga gcctcacacc tcactagggtg cagagagccc720
aggccttatg ttaaaatcat gcacttgaaa agcaaaccctt aatctgcaaa gacagcagca780
agcattatac ggtcatcttg aatgatccct ttgaaatgtt ttttttggtt ggtttggttt840
aaaatcaagc ctgagggtgg gtggaaacag gtagcctaca caccctaaat tgggggtggt900
cccgggggaa tggtt

```

(2) INFORMATION ON SEQ ID NO. 115:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 685 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

004227" 562960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

gaaaatccag ggggtgaagaa tagatctgtg gtggcagggg tgggaaaggc ggggaggatt 60
tgcctactga ggggcagcac aagagaattt tgcggggcga tggatctgtc tgtatcttga120
ccatagtgat gatacatgac tgtgcatttg tcagaactca caggactgaa tgaaaagaga180
agtgaatttt actgcatgtg aattgttaaa ataaatgcta gacagtattt taaaaatcaa240
gccagatcc tgcaagacat tatggctccc caccagaagg ggagagacgg ggaaagagaa300
gtgtccccaa agttaacca cgttccctgg gaccacctc cctccccact gccacttccc360
accagcctca cgcacggggc aggcccttcc ctttgcagct cacagcccag cagatgttag420
gtcagaatgc gtccccctcac ttgactaaag gtttacagcc agcagggtgg gaaatgaacc480

agatattaac accccctcct ccatgccctg ccacaccttct gggccagtac cagtgaaggc540
aggaagccac ttctcccacc cccaggctgt tcccaaagcc ctggaagaac ccaaggaaag600
gcaggagcca agttgggagt tgaccttgat gaccaggggc cagttggccc agtttccctt660
gtttagttgg ggggagggaa ccctt                                     685

```

## (2) INFORMATION ON SEQ ID NO. 116:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2646 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

ttaatttaaat agctttcatg tgattaaaaa tagctaacta gactcaagga ttcacaatat 60
ttaggtgtat tttcaatacc tccagaaagg aaacctcagt taatcagagg aaatagtttc 120
agtcttcatt tgagcatgtc tttccatctc aaaaaaatac tcttagtagg ttggagtga 180
gatagcaagg ttttgaagca tatttgtcct aatccacagt gacacttttt atcttccagg 240
agcactccta ggaggttccg tgcctaataca atgttgactg ctttgcagat ctcaaggga 300
taaaatgaca aaagcaggga aagttacaga ttcaaacagc attttaactc atgttgatct 360
ggataattaa tcttttctaa agatgtgtag tttcttgga aacagtgata tcacatgatt 420
aaaattacat ttttatcaac ataattgtct ggaaaagata agcccctcaa tttctacca 480
gttgactttt attcattaga tacagaagggt gcagatttac acatcaccag ctgcccttgt 540
gaatggctca ctacacagcc attgggttac aactgtgtgc atgggcagaa acagcaagt 600
ccctcattgt ggtcattggg tggggagtgc cttttgtcaa ggagtctgca ggaattggct 660
tatttctgta tgccaaagt atcaacacac caaagtctct gccataaaga atgtggcttc 720
cttgcatcct ccacctgtt actctgggccc cagtaatttg atgtaactgt ctgattgtac 780
tagagacagg agtatacca gcttattcat aatcaagtaa agagactcag attagatttg 840
attttttagc ctctctaga gccaatcagg cagttaagag taataaagga aaagggttg 900
gtcacaacc ctaccattat ctggagatta ctctctgctg cactcctgtc ttgccatgca 960
cgtcttgccc cctcattttt gctcagccta gcagtcact tcactttatt gccttgtaag 1020
tgtcaggcct cctgggcgct ctggaaaaga cagggagcca ggccctctca cccctactgg 1080
taacaggcca ttgctgggtg cacaagagggt aggtgatttg catcatggtc atgctgcatg 1140
ggcttcactg ggatgctgtt aaacaccaga ggagccaacc tatcagaatc ccagcagca 1200
aggaaaactc agattttaga ggctttttac aataaagtag cgtaactcta ggtcatgatt 1260
gatttcaaat gcctgccatg aatgatttgt aagtaattat gtaggatcca tcaaagcagt 1320
attgtaggct tttgaattgt cccagtggt cggggaccoc atttactgt ctctcttgat 1380
cgtgttaatg atgcaatcag agttcaagac agggcccatg aagtctgact gcactgggat 1440
ggagaaatga atttcttccc actgaaggaa actctttctc attcgagcc aagacgggag 1500
tgccactgtt cctctcttca ctctgagat actgctctg gaagcgggtg tcacttctct 1560
tctagtacct cttctcttct ctgaagtgtg tgactatctc ctagtgttta aatttggcag 1620
ttactcgcca tgtatgtcag catagaaaag gaaatgtttt taccttatct cctgtatgta 1680

```

```

tgatagaact taaaagaaat gtgcatttgt tttcatagcc ccagcagaga aaatcctctt 1740
catagattaa atgtgctgct gtggacagga gggaaaaaaa aacctctac atattgaaag 1800
gcaccaaagt taatatctga cactgttaag atgcccacaa gagcaaagt gttagtgaga 1860
tgcagggtca tttcccatg ccacccacag tgtttgttag tgagtccacg gctgacttgc 1920
agtgataaag aaaagcatgg agctgtgtct gcagacaatg gtggctgcat ctgtaagtgg 1980
cttcagaggc agcagccctg gggaaattga tgggtgtggc agtggacctg tgaagaggga 2040
gaatctagcc ttcagcctgt ccagtgttaa ccactagaga aactgagctt tatatccttt 2100
tttaatgcct gtgaatttta gcatattgaa acattagagc aaataactcag gggatttttc 2160
attaaacatc cctcagataa tttagctata tatcattaga aagggaagc tatcattttt 2220
attttaaaac taaacaaggc catcttataa actgtcacca aagtcttccc tttttatttg 2280
catgtgtgcc ttgaatttca taaaacatta attcacaatg ggggtcagaa tgtactcttg 2340
ttgaaacact tcttgtagca ttttatgttc atattatgtt tgagagggtg aaaatgtatg 2400
agcagcttaa ctgaagtaga actattcatg atgcttttca cacattgtgg cataagatgt 2460
aaagtgtgta attaatgtta atttctgtgc attttaatat tcttttataa ttattaatgt 2520
taatttctgt gcattttaat attcttttat aattatgagc attttaataa attcattttt 2580
acaaacaata aaaaaaaaaa aaaaaaagg ggaagggaag aggaagaagg aggggggaag 2640
aggaag
2646

```

## (2) INFORMATION ON SEQ ID NO. 117:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2667 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

ttatcttgga agtctgtgta tcaaaatgaa gaattcagat ggtaggaggt tctatagtcc 60
ttttaagct gactcttgag tgtcagttga atatccatta aattggattt ggaaataacc 120
tgaggaaagt attatgaatt cgatctgcac agatgcctct tagctgatag gtggcaggcc 180
tgtgggtttg ggttctccct cttttctctg gaacatatga caattccaga ttaaagaaaa 240
atgtttttta ataaataccc ttggtctttc ttctagtcac ctttgaggta gatattgtga 300
ttttctggag tatagtatat ccgtgtctct gtgtcttagg ttactagat gcaataatac 360
ttctctttga catttggtact gaagtgtatt gatattaagt aaaacagtta atgtttgaat 420
ataggcatat ttataggttt ttccgctcc cccccaacc acccttttta aaaaatctat 480
acaaagccct tgtttgagtc tcatcatgca catcaaatca tggagttagg tcttctctga 540
gctcagggga acacaagtgc acagagagag atgtcttgag ggtcactacc aaagaattac 600
cctcattgtc cctcactcag gccatgtgta catgcgatgc tgctgagtgt gctggggtgg 660
gtggtggcca cgtggctccc ccagagcaact tcctaactgg caagctggga gaccattac 720
tggtgaactt tgtggaaatt agaactgta cttttacata atcttggcat attacatttc 780
ataataaaaa catacattta gttgcatgct acatcactat tgattttata attaatcttct 840

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002227"56EE2960

```

taagcttcaa ccatgtttta taccttattt cgttacatca tatatttgta atgtgtaata 900
tgaaatcttt tgctttaatg tcttttttta aaatgtagaa tgttctaaac ttgaaaggca 960
attgaatgta gtatgatgaa aatgtgaatg ttttgctgct ttcacgacca aagatacagg1020
gctagtggac atttagaata ataattaaag ctagagtctt gtatgtcttt tctttgaagg1080
agttctaacc ttgtaaattg agaatgactt cagagaattt tgattaagaa aacattaaaa1140
tcttaaccgg cacaacact ccaatttttt tcaactgtgaa gccgcaagca attttttttc1200
tttttctttc aaaagcctgc cttctgaatt tatttcttgt ttactcattt cagagagggt1260
agtaaagaag atctatttct ggtagtcata tcgcttgaaa ggtattggta aatgtgtttt1320
cagtcgtgac catgtggaaa gtgaacagtg ttggcaaaca ttaccgagaa aatcatgctt1380
ttcaagatgc ccttgctttg ggatatcctt cctagggaga aaaaaaaaaa gtagtttaac1440
aattgtgaat tccatttctt atttcagttt ctgctgcagt aatgggttcc caccactat1500
aattcccagc atttatgttc tgttgatttc tccccttagc ccagtaacat ttttatcta1560
taccatcttc cccaagtttt gagacagatt gacccctac tcattatgtg gctctagttg1620
aattttaaaa tgtggaatat tgggcttgca ggcagtagga gctgcaaate tggtagagt1680
ggagtgtgga gttaatggtg agtatgttaa taaagggaaa ctgtctctga cagaatctca1740
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ctcagctaca ggctgcagtg caaacttttc ttccatccag agaaagcaga attccctcct1860
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tatttgtgcc atctcttgat gactgatgac ctggatcgag tatttctatg aagggtcttc1980
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gacaccagga gaagtatac ctagggttac tgagcagctc atcatccctg tttctgcaca2100
gtttcctgaa aetggccatc agggcctctg aggcactcaa atcagtttac ttttagcatg2160
cccccatcag ggtgggtctc actgttagtg aggatacggg tctgggttga tgtttttcta2220
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aaaagggaaat tttcatgatt tgatttagat tagtatttaa atatctgctt tagatagcaa2340
ttaattttat tgtaaaaaata aggaaaaata tgtgaatatg tgaatttttt aagcctgaga2400
gatgatagaa tgttcccata tttttcttgt aaagaaaata atattttaac ttacacatcc2460
tgtagaaaaat accacctttt ccccttgat tacagtacaa tgtttacatt actatactgt2520
caagctgaaa gtataaaaaa tgtacatata cattttgagt tatgtatcct ttttttaaaa2580
aaaggtgcgg ggctgtggca ctgggctgga catgactaaa gttgacagag gctatgctag2640
atttataatc actagtctctg ggacttg

```

2667

## (2) INFORMATION ON SEQ ID NO. 118:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 544 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

0967395-122700



(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```
catctgtgca tggatgagtg gccgactttg gagcccaggc tgttacttcc tgggtctggtg 60
gtgaatcctc catagtctga gagtaagatc cttgatactg gctcagcatg gaacatctgg120
cacacagtat gcactgagga aatacttggt ggaataatca gtgaatcata gatgaaaact180
taaccttgga attaattatg agactgctca gaggaagaga atgggagaca aaggacctgg240
tgattagacc cccaagacac tgggctgtct gcttgtgtct cgggtggaac aggcccagcg300
agagtcttta gggccagaac tcaaggaatt tattgagcca tggcaaacag gcagtaaaca360
gccattctg gctgctgtat tgagaagaga atgtggtgga cagatataga agcatggaaa420
cctgataggg ctattgcaat cactcagaaa agaggcgatg gcagcttgga cctgttgaag480
cagtagagtg ctttccaggg aggagaaaagg acctgaaggt taatttgatc accatggggc540
atga
```

544

(2) INFORMATION ON SEQ ID NO. 119:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1340 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

0967395-12700  
002221-5662960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

gtttgatact ttcctgcact taggtttgtc ctattcttca tttattcaga ctaggataga 60  
 aaattttgga atcagaaaat agatccagtg tttagctaca tacaatctag tacaagtga 120  
 tttttattct taaacatagg tgtgttggt ctttttttaa aagatgcgct ctacctgaaa 180  
 aggaaattgg attttagaac tggatgtggt gcagtgaagt attttaggcc caggtctgtg 240  
 tacacatttt atagaagaaa tgaagtactc tgaagtattt tgggtgcctt ttcatttcaa 300  
 ctgtgttttg aatttgtcag atcacacata tattgtgtta ttgggcgctg tggatatctt 360  
 tataaaacct cttgcttgtg tgcaaaagtt cctaaaagga aacacaagta atgcctatcc 420  
 attactagca tgctatgctg catgctttac tgccattgct gtatgcttta ctgtctttgt 480  
 aaaaatcccc ctctcccctt ttctggtaac tggaaaagca tgctaaaaat agtcttatat 540  
 tttcacccca taagtgcaga atcagtaatt ccttggctta aagctcttat ataataca 600  
 ttattggtgg taaataccaa gtttgggtat tcatagctat ctttttttaa agaaattaag 660  
 ttcttgaaaa ttttagccaa tcccgtttta tgggaatgct ctttagaatt cattttgttc 720  
 agcccccttg ttctatggtt gagaaatctg aggccttacg aagggttaaga gaactttccc 780  
 cgtgtctcac aggtaggtag aggcagagct ggaactagat atctggtctg ttgactctag 840  
 ctacgtgtct tctggtaact gttgaaaatt gtcttagttt gagagatggc tgaataatg 900  
 aacataaaat gctatttata ataacaagta tatgtgaaat ttcttattgt aagactacta 960  
 ccggcttact gttgaatagt ttggttatag tgtttaggct agaaatgcct cccacattgg 1020  
 taataaacat tacaaaatac aatgtatttt taggtaggca ttttataaaa tgcattatgc 1080  
 catggttgct tttgagatag attgtagtct gggtagcatc tttaaaatgt atgtgggctt 1140  
 aactgttggt catatcagga gatgctctga ttgtataggt gagactctgt ttctgttatt 1200  
 ttttaattgt gtatgaaatg tgatcagatt attttactac caacagttat agtttgaaag 1260  
 tccaactgta ttaattgact gataatatga taatatagag attaaattgt ttgtcttcat 1320  
 tccttaaaaa aaaaaaaaaa 1340

## (2) INFORMATION ON SEQ ID NO. 120:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2376 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ggatatgaat aaattgttaa tataaagtcc tacagaaatt aatttatgaa atttctctaa 60  
 atcacacaaa acttaaatac agatgactac taccctgaga ctgaaaaata tgttctaatt 120  
 tatagtgcta tttttgggca gttttggtgt cagaatacct atcaacacat tcttttttta 180  
 ttaggaaaaa aaggatgtct acataacaat ttgtaaagt ataaaatcca ttagttttta 240  
 agtcttctga tagcattggc tattataaga aacaagtatt tgctctcgtt tttaacggga 300  
 taataatgct atgtctacat aaaatgattt ctaccacctt aaatagctca ctgtagaaat 360  
 tcatgtataa atggaaccat atagtacata catatcatat tcttaggtct ggcaaatatt 420  
 tgaggttcat ccatatttta tattcactca tcagtagttg taaacacatt cttaaagtag 480  
 ctttttcaga tatgaataag cagggatgaa ataagtatta gggtaaggga aatggttgag 540  
 gctttcctaa gtgaagtgt aaaaaccacag ctttcttttt aatgggatgt ctaatatgca 600  
 tttatctgtt caagcatttt aagatttcca tgaaaatgtc ctgaaaaatc aagattcttc 660  
 attgaggggtg aggatctccc aatgggagac tgctctgaaa agagcatgtg ctttttgaat 720  
 tagataacct actataatca tggatgttct tgaatactta gcaaacatac cagcatccca 780  
 aagtcaccaa gataaacctt cctactccaa catcacatga tcttctaatt ctacctgtaa 840  
 aaataagcat aacaattaat tagaatataa ttacgttata tacattactc cacctagaaa 900  
 aaaaaatagt tcattatgta gagaaatgct ttttttagta catagagaaa taaaaaatat 960  
 agatactcac tagtgaacaa aaaatgtcca aagccagcca caacagatcc taatgaacca 1020  
 tacaatattg aatgccgggc gcagggagta ttttcaacat ctaaaaaatcc taggagctta 1080  
 agggactaga atgaaaaaaaa agaacctaga ttgagtaaga aagtatttca ttttgggggtg 1140  
 ctttggcaaa aatgacaata caccatttct tttctttagt ttgaggggtt aaactagagt 1200  
 atgtgccacg tgacaacctt aatcagcttg cgttgtcttt gtccaccttt ggtatgcagt 1260  
 ctgaatcttt aaatccgaaa accttataaa ttggaccgga aaacctttaa gcagtagggt 1320  
 aacttggagc tgtatcttaa tttgctaate aactgacttg gaaataggat aattcatttt 1380  
 atgagctctt taaatgagtt tatttgggaa tatgcctatc attggaattg aaagcagcat 1440  
 agcttgcttc agtaactcca ataatttggg aagcagaaat ggaaaaagta atttgagtca 1500  
 tgtttgctta tgtagtgcct tttaaaattc ccctagtaat tacctttcat attttattaa 1560  
 ctaggttaac atcaactgtg gttgtaagag taaatgtttc accttaagat aaacatgggc 1620  
 aatatattaa actctagtct gttttcttgc ctgtgaagtg aggctgcact tgattatatt 1680  
 tgattctttg ttcgtaatac atgggaacga cagctaagtg tggtgaaaaa cgcggggatc 1740  
  
 caaagagctg gatttttatt tcagatctgc cgctaacttt tgtatcctat aggctacttt 1800  
 tatttctatg gtctcaatct ataacatgaa tgggttgggt taaatgactg aagttccttc 1860  
 aagtgtataa attctttttc tacagtcttc attggattta tgtatttctt attcctaata 1920  
 tgtttaactg ggatgtctgt cactctaggg cggcaagaca gacattttaa agtaacagtc 1980  
 acactgctga actggcattt ctgttaacac aaaagtttag aaaactcacg gtaactgtta 2040  
 cttgatttaa gtgtatataa aattttcagt aaggctgctt ttaaaaggaa ccactgtcca 2100  
 tttaaagggt tcatagttat cttcaatggg ttagtattgt ttggggcagg acattaaact 2160  
 agaagggatt ctataggatg aggtgatacc tagaaggtaa tatattgtaa ggcaaaagag 2220  
 attagaagaa atggggggaa aggatagtaa aaggcaagtc agattaaagg gttgaaacat 2280  
 gaagatatcc ccattgtatt cgggccccat gtttgccctt tttggctcca gcatcgtgtt 2340  
 tggaagaggg caatgtgccc tgggtcccta ataaag 2376

002221"56E2960

## (2) INFORMATION ON SEQ ID NO. 121:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 225 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```
cagttgtgaa gttttgtaaa atggtcaccc aacttaaaac taggaaatta cgaagaagag 60
aaaattgccc ggtatctggt aaggtctgcc tgtagatctg ctgtagggct tgtcaccatt120
ggaagcaagg tctacttca gtggcagatc ttgtggcctt tgagtggctg aagaccacca180
ccctgcacag ggctggggcc atgcacaggc atccttcctt acctt 225
```

## (2) INFORMATION ON SEQ ID NO. 122:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1967 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227 5652950

acgggcggcg	cccgcgctcg	caggccaactc	tctgctgtcg	cccgccgcgc	gcgctcctcc	60
gacccgcctcc	gctccgctcc	gctcggccccc	gcgcgcgccg	tcaacatgat	ccgctgcggc	120
ctggcctgcg	agcgtgocg	ctggatcctg	ccccgtctcc	tactcagcgc	catcgcttc	180
gacatcatcg	cgctggccgg	ccgcggctgg	ttgcagtcta	gcgaccacgg	ccagacgtcc	240
tcgctgtggt	ggaaatgctc	ccaagagggc	ggcggcagcg	ggtcctacga	ggagggctgt	300
cagagcctca	tggagtacgc	gtggggtaga	gcagcggctg	ccatgctctt	ctgtggcttc	360
atcatcctgg	tgatctgttt	catcctctcc	ttcttcgccc	tctgtgacc	ccagatgctt	420
gtcttcctga	gagtgattgg	aggtctcctt	gccttggtcg	ctgtgttcca	gatcatctcc	480
ctggtaattt	accccgtaga	gtacacccag	accttcacc	ttcatgccaa	ccgtgctgtc	540
acttacatct	ataactgggc	ctacggcttt	gggtggcgag	ccacgattat	cctgatcggc	600
tgtgccttct	tcttctgctg	cctccccaac	tacgaagatg	accttctggg	caatgccaa	660
ccgaggtact	tctacacatc	tgcctaactt	gggaatgaat	gtgggagaaa	atcgctgctg	720
ctgagatgga	ctccagaaga	agaaactgtt	tctccaggcg	actttgaacc	catttttttg	780
cagtgttcat	attattaaac	tagtcaaaaa	tgctaaaata	atttgggaga	aaatatTTTT	840
taagtagtgt	tatagtttca	tgtttatctt	ttattatgtt	ttgtgaagtt	gtgtcttttc	900
actaattacc	tatactatgc	caatatttcc	ttatatctat	ccataacatt	tatactacat	960
ttgtaagaga	atatgcacgt	gaaacttaac	actttataag	gtaaaaatga	ggtttccaag	1020
atttaataat	ctgatcaagt	tcttgttatt	tccaaataga	atggactcgg	tctgttaagg	1080
gctaaggaga	agaggaagat	aagggttaaaa	gttgtaaagt	accaaactc	ctaaaagaaa	1140
tgcaaaaaaa	aagtttatTT	tcaagccttc	gaactattta	aggaaaagcaa	ataacattcc	1200
taaatgcata	tcatttgtga	gaatttctca	ttaatatcct	gaatcattca	ttttagctaa	1260
ggcttcctgt	tgactcgata	tgtcatctag	gaaagtacta	tttcatggtc	caaacctggt	1320
gccatagtgt	gtaaggcttt	cctttaagtg	tgaaatatTT	agatgaaatt	ttctctttta	1380
aagttcttta	tagggttagg	gtgtgggaaa	atgctatatt	aataaatctg	tagtgttttg	1440
tgtttatatg	ttcagaacca	gagtagactg	gattgaaaga	tggactgggt	ctaatttatc	1500
atgactgata	gatctgggta	agttgtgtag	taaagcatta	ggaggggcat	tcttgtcacal	1560
aaagtgccac	taaaacagcc	tcaggagaat	aaatgacttg	cttttctaaa	tctcagggtt	1620
atctgggctc	tatcatatag	acaggcttct	gatagtttgc	aactgtaagc	agaaaacctac	1680
atatagttaa	aatcctggtc	tttcttggtta	aacagatTTT	aaatgtctga	tataaaacat	1740
gccacaggag	aattcgggga	tttgagtttc	tctgaatagc	atatatatga	tgcactcgga	1800
aggtcattat	gattttttac	catctcgact	tacataatga	aaaccaattc	attttaaatat	1860
tcagattatt	attttgttaag	ttgtggaaaa	agctaattgt	agttttcatt	atgaagtttt	1920
cccaataaac	caggtattct	aaacttgaaa	aaaaaaaaag	tcgacgc		1967

## (2) INFORMATION ON SEQ ID NO. 123:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 612 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```
cctagctgtc cccctgagat gaagaaagag ctccctggtg acagctgcct gccccgctca 60
ctcgagcttc accctcagaa gatggatccc aagagacagc acattcagct cctgagcagc120
ctgactgagt gcctgacggt ggacccccctc agtgccagcg tctggaggca gctgtaccct180
aagcacctgt cacagtccag ccttctgctg gagcacttgc tcagctcctg ggagcagatt240
cccaagaagg tacagaagtc tttgcaagaa accattcagt ccctcaagct taccaaccag300
gagctgctga ggaagggtag cagtaacaac caggatgtcg tcacctgtga catggcctgc360
aagggcctgt tgcagcaggt tcagggtcct cggctgccct ggacgcggct cctcctgttg420
ctgctggtct tcgctgtagg cttcctgtgc catgacctcc ggtcacacag ctccttccag480
gcctccctta ctggccggtt gcttcgatca tctggcttct tacctgctag ccaacaagcg540
tgttccaagt ttactcctac agtctgcaag gttacagggt gggtggggga gaaatgccgt600
tttggggttc ca                                     612
```

## (2) INFORMATION ON SEQ ID NO. 124:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1183 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

004227 5552960

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

tttcggcaca gcatgaatgg ctgcgagaag gacagctcgt ccacagattc tgctaacgaa 60
aaaccagccc ttatccctcg tgagaaaaag atctcgatac ttgaggaacc ttcaaaggca 120
cttcgtgggg tcacaggccc aaatattgag aaatcagtga aggatttgca acgctgcacc 180
gtttctctaa ctagatatcg cgtcattgatt aaggaagaag tggatagttc cgtgaagaag 240
atcaaagctg cctttgctga attacacaac tgcattcattg acaaagaagt ttcattaatg 300
gcagaaatgg ataaagttaa agaagaagcc atggaaatcc tgactgctcg tcagaagaaa 360
gcagaagaac taaagagact cactgacctt gccagtcaga tggcagagat gcagctggcc 420
gaactcaggg cagaaattaa gcactttgtc agcagcgtga aatatgacga ggagctcggg 480
aaagctgccc ggttttctcg tgacatcgaa cagctgaagg cccaaatcat gctctgcgga 540
gaaattacac atccaaagaa caactattcc tcaagaactc cctgcagctc cctgctgcct 600
ctgctgaatg cgcacgcagc aacctctggg aaacagagta acttttcccg aaaatcatcc 660
actcacaata agccctctga aggcaaagcg gcaaacccca aaatgggtgag cagtctcccc 720
agcaccgccc acccctctca ccagaccatg ccggccaaca agcagaatgg atcttctaac 780
caaagacgga gatttaatacc acagtatcat aacaacaggc taaatgggcc tgccaagtgc 840
cagggcagtg ggaatgaagc cgagccactg ggaaaggcca acagccgcca cgaacacaga 900
agacagccgc acaacggctt ccggcccaaa aacaaggcg gtgccaaaaa tcaagaggct 960
tccttgggga tgaagacccc cgaggccccg gccattctg aaaagccccg gcgaaggcag1020
gcacgctgca ggacacctcg ggagggccag gggcctttcc ggggttagtt ttcggtagg1080
ggttttcaca gttgcatttt tttgccccca cggaggatta ggaagttttt ccacagatgg1140
caggcatttt ttttgagttc cccggttttt gacgttttgg ttg 1183

```

## (2) INFORMATION ON SEQ ID NO. 125:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 891 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

004221 5662960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

cggaggcagc ggaaagccga gccaggcgcc tgcgcgctgg gaagagtagg ttcagagtgc 60  
 attccggaac ccggggcgcg gcgcactgcg caggcgcccg gactccgctc agtttccggt120  
 gcggcgaaaca ccaaagtcg ggaacttaag cattttcggt ttctaggggt gttacgaagc180  
 tgcaggagcg agatggaggt ggacgcaccg ggtgttgatg gtcgagatgg tctccgggag240  
 cggcgaggct ttagcgaggg agggaggcag aacttcgatg tgaggcctca gtctggggca300  
 aatgggcttc ccaaactctc ctactgggtg gacctctggc ttttcatacct tttcgatgtg360  
 gtgggtgttc tctttgtgta ttttttgcca tgacttgttc gctgatatct aaattaagaa420  
 gttgggttctt gagtgaattc tgaaaatggc taaaaacttc ttgaataaag aagacaggac480  
 tctcaataga agaatttcac atctccaagg gaccttctct ttcattttac actttgttac540  
 taatttgcag aactctatta attgggtagg atttcaccca ttcctagcta agttcttaaa600  
 attaaaccct ttggttcgtg tttaaaaact ttcaaacatc tgatggcttt acaggggctg660  
 aatataaaag catttgtact taaagggtctt gtgtattcat taagaaatat agtaatgtct720  
 tttaatgttt taagagttga tcaggggttt actatggatt gcaagtaata gggatgatta780  
 ataaggggaa ggtttttatg gaatttcaaa agtcaattta tttcaaaagc gggggaaagg840

gttttgagag gagggggggc caagggtgttc ctgggggtttg ccgaggggagg c 891

## (2) INFORMATION ON SEQ ID NO. 126:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 482 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

tctctaaata gtaccttttc agtcttgccc cagaagttcc ctcaatttca gcagcaccga 60  
 gcgggtttata attcattcag ttttccaggc caggcagccc gctatccttg gatggccttt120  
 ccacgcaata gcatcatgca cttgaaccac acagcaaacc ccacctcaaa tagtaatttc180  
 ttggacttga atctcccgcc acagcacaac acagggtctgg gagggatccc tgtagcaggg240  
 gaagaagagg tgaaggtttc gaccatgcc a ctgtcaacct cttcccatc attacaacaa300  
 ggacagcagc ctacaagtct ccacactact gtggcctgac aacagaactg agaggagagg360  
 attagactct ggggtgcttg catgggcaac tggatttttg catgattcct ttatgatttt420  
 gcttttaatg tatacacc a gaagagccaa tataaacgtt cctcatgcct aaaaaaaaaa480  
 aa

482

007227 5657950



## (2) INFORMATION ON SEQ ID NO. 127:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 610 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

ctcgagccgt  gggcagtggc  cgcgaatgcg  cggagacact  gaccttcagc  gcctcggctc  60
cagcgccatg  gcgccctcca  ggaagttctt  cgttggggga  aactggaaga  tgaacgggcg  120
gaagcagagt  ctggggggagc  tcatcggcac  tctgaacgcg  gccaaagggtc  cggccgacac  180
cgaggtggtt  tgtgctcccc  ctactgccta  tatcgacttc  gcccggcaga  agctagatcc  240
caagattgct  gtggctgctc  agaactgcta  caaagtgact  aatggggctt  ttactgggga  300
gatcagccct  ggcattgatca  aagactgcgg  agccacgtgg  gtggctcctg  ggcactcaga  360
gagaaggcat  gtctttgggg  agtcagatga  gctgattggg  cagaaagtgg  cccatgctct  420
ggcagagggg  ctcggagtaa  tcgcctgcat  tggggagaag  cttagatgaa  agggaagctg  480
gcatcactga  gaaggttggt  ttcgagcaga  cagaggggtc  tcgcagataa  cgtgaaggac  540
tgtggcaagg  tcgtcctggc  ctatgagcct  ttttttgggc  catttggtgc  ctggcaaggc  600
cttcaaacag

```

## (2) INFORMATION ON SEQ ID NO. 128:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2072 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

002227" 5652960

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```

gggtcatgta ggtacaacag caaccaagaa gatcgatgtc tacctgccct ctgcaactcga 60
gccaggacag actgctgcc aatgacctgg tgacaatggc cagcgccagg gtgcaggacc 120
tgatcgggct catctgctgg cagtatacaa gcgaaggacg ggagccgaag ctcaatgaca 180
atgtcagtg ctaactgcctg catattgctg aggatgatgg ggaggtggac accgatttcc 240
ccccgctgga ttccaatgag cccattcata agtttggctt cagtactttg gcccctgggt 300
gaaaagtact catctcctgg tctgacatcc aaagagtcac tctttgttcg aataaatgct 360
gctcatggat tctcccttat tcaggtggac aacacaaagg ttaccatgaa ggaaatctta 420
ctgaaggcag tgaagcgaag aaaaggatcc cagaaagttt caggccctca gtaccgcctg 480
gagaagcaga gcgagcccaa tgtcgccgtt gacctggaca gcactttgga gagccagagc 540
gcatgggagt tctgcctggt ccgcgagaac agttcaaggg cagacggggg ttttgaggag 600
gattcgcaaa ttgacatagc cacagtacag gatatgctta gcagccacca ttacaagtca 660

```

```

ttcaaagtca gcatgatcca cagactgcga ttcacaacog acgtacagct aggtatctct 720
ggagacaaaag tagagataga ccctgttacg aatcagaaag ccagcactaa gttttggatt 780
aagcagaaaac ccatctcaat cgattccgac ctgctctgtg cctgtgacct tgctgaagag 840
aaaagcccca gtcacgcaat atttaaactc acgtatctaa gcaatcacga ctataaacac 900
ctctactttg aatcggacgc tgctaccgtc aatgaaattg tgctcaaggt taactacatc 960
ctggaatcgc gagctagcac tgcccgggct gactactttg ctcaaaaaca aagaaaactg1020
aacagacgta cgagcttcag cttccagaag gagaagaaat ccgggcagca gtgacactgg1080
cctccagcct caatctgttc cgtagctcag agcctgcctg ccagggccaa gtgccctagall140
gcccacccgg tgtcctgaag tctcggggg gaggccagcc cctggctcac tggcacagggl200
caggtgggct ctcggggaag gtgtcggggg cccctagga gggagcgctg gggacattgc1260
catgggacgg aagtctgctt ggcagtggtt ttgataagcg atgcttgggg gtcagaccac1320
cccctagagg agccacgtgc cgcacagcca ccttcaatgc ctgccaccct gcccgaggat1380
gtacagagcc gtgcccacac atttccctgc aacttgatca aatttcttaa agcaaacac1440
aaaaatgtac atttctgttt ttccctttta taaacagggt tactctttat catggttgggt1500
atgatggacc attctttggg gcggaggatt gattatgtta ctctctttta aatctgttcc1560
catattgaac aggcagattg gaaaagctat ggttcgattt ctcagaagaa atgtttaggt1620
cttagtcaat agttttaact atgccatttg tttaaatgag tgcatttgct tcgagggtag1680
tgtcttacta aaagtttagga acagagacct agtgggtgtg ccaaggccgt gtcactttcc1740
ccttcagcac accccagctt ctgacctcag agcccaggag ctgcgtggac agtgtgggg1800
gccaggagga ggggcgggtg ctggtcctca ggcacgctgc actcccagcc agacatggtc1860
tttccgtttc ttaagtagca agtgtaggtt tcagctggca gttccacctg catgttctct1920
gcttcgctgc ctgggaaggg gccacattcc ccattcctct tctccttaca gcgcctgect1980
cctttttaag caggcggaag gctgctgttt ctacagtttc agggagaggg gtgaccagga2040
gactgtgtcg tgcgtcggtc ctgggtggac ag
2072

```

002221 5554360

## (2) INFORMATION ON SEQ ID NO. 129:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 980 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```

tttatggagt tagagcaggg gaacttaaaa acaaaagtgt atttaataac ttcattgagac 60
tgtgataacc agtttatatt tgaaatatat acagcacttt gggagactga ggggtgaccc120
tgatagtcct ttgcacagtg atcttcagat cttaaaagaa aaagaaggca tagaatatat180
tttgcttaac ttctctttta aggataactt tccatttgat cctccatttg ttcgagtggt240
gttacctggt ctctcaggag ggtatgtatt ggggtggagga gcattatgta tggaaacttct300
cacaaaacag ggctggagca gtgcctactc aatagaatcg gtcattcatgc aaataaatgc360
caccttagtc aaaggcaaag ccagagtgcg gtttgagca aataagaatc aatataatct420

agcaagagcc caacaatcct ataattccat tgtacagata catgagaaaa atggctggta480
caccctcca aaggaagatg gctaaatatg ttgactgttg tatgtttgga ctaatgttgc540
tttaaagaaa atctttccaa catgcagaca aaagctttga gtgcccctat tacagcagta600
ccgaagatgt tagttaatag atatttttagt ggataatctg tcattctgaca tccagtataa660
gttacagcct tcgcattttg ctcatcttag atatcttgga ctgagcagtg gggcctttac720
tgtatttttc ctgataaata cacatactgg ccactcctta tctctttttc ttgaaaagt780
aactttttaa aggcagccaa gtcaacatca' gggctactga agttggaggg ctttaggggt840
aactttccta tattgagccc atgggggttac aagggtttgg caatatattg ttccctttta900
cagccaatac aggtttttaat cggatgtttc aatattgggt ttaggggatt ttaaggggccc960
tcttaagtca taatagccct                                     980

```

0967395-12700

## (2) INFORMATION ON SEQ ID NO. 130:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 792 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```

ctgttttgca gggcggggcg cctcgcaag atggtggcg gcgcggcg tggtcccgt 60
cgtctggcca agtctcagcg cacgcaaccg gccggcgctc cgttggcctg gagccacac120
ccaccgggtc cctgaccccg cgcccccg gcccggttc cgcatgcct cgcgccgta180
agggaaacac gctccggaag ggtggtcagc gccgtggagg aggtgcccg agcagtgcc240
aagctgactc gggttccagt gacgatgagg cagccagtga ggccgcagc accgccagt300
aatgccccag ccttctcagc accactgcag aggacagcct tgggggggat gtcgtggat360
agcaagggcc agcaggaaga ccttgaggaa aagctgaagg agtatgtgga ctgtctcaca420
gacaagagtg ccaagacccg gcaggtgcct cttgagagcc tgcgcctggc cctagcgtcc480
cgctactcc cgcacttctt gctggagcgc cgcctcacgc tagccgatgc cctggaaaag540
tgcctcaaga aagggaagg cgaggaacaa gccctggctg ctgctgtgct aggctgctc600
tgcgtgcagc tgggccctgg acctaagggt gaggagctgt ttcacagcct gcagcctctg660
ctggtctctg tgcctcagtga cagcacagct agccctgctg cccggctcca cgtgagttgc720
ctgtgcccc aaaaaccctt cctgcaact atccctcagc agagtgggtg gttcccccta780
tcttcagcct cc                                     792

```

## (2) INFORMATION ON SEQ ID NO. 131:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

004227 5554960

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

gtgggtcccc ccggttccgg cgcggttgag gccttcggtg gtgaacgagt ctccagcacc 60
atgtctggtt tgtctggccc accagcccgg cgcggccctt ttccgtttagc gttgctgctt 120
ttgttcctgc tcggccccag attggtcctt gccatctcct tccatctgcc cattaactct 180
cgcaagtgcc tccgtgagga gattcacaag gacctgctag tgactggcgc gtacgagatc 240
tccgaccagt ctggggggcg tggcggcctg cgcagcacct caagatcaca gattctgctg 300
gccatattct ctactccaaa gaggatgcaa ccaaggggaa atttgccttt accactgaag 360
attatgacat gtttgaagtg tgttttgaga gcaaggggaa agggcggata cctgaccaac 420
tcgtgatcct agacatgaag catggagtgg aggcgaaaaa ttacgaagag attgcaaaag 480
ttgagaagct caaaccatta gaggtagagc tgcgacgcct agaagacctt tcagaatcta 540
ttgttaatga ttttgcctac atgaagaaga gagaagagga gatgcgtgat accaacgagt 600
caacaaacac tcgggtccta tacttcagca tcttttcaat gttctgtctc attggactag 660
ctacctggca ggtcttctac ctgcgacgct tcttcaaggc caagaaattg attgagtaat 720
gaatgaggca tattctcctc ccaccttgta cctcagccag cagaacatcg ctgggacgtg 780
cctggcctaa ggcacacctac caacagcacc atcaaggcac gttggagctt tcttgccaga 840
actgatctct tttggtgtgg gaggacatgg ggtaccacct acaccaaca agtcaatgag 900
ggacttcttt ttaatttggg aggatcttga ctgggtttgc aacaataggt ctattattag 960
agtcacctat gacaaaaaat aggggggttac ctagataatg ccaaagtcag catttgtccc1020
gggtcccttt gtgggagctg tgggacgatg ttttcttttc tgcccccttt cgggagcgtg1080
gggggccaaa ta 1092

```

(2) INFORMATION ON SEQ ID NO. 132:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1523 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

002221 55552950

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

ctcatgtcta aagaaattcc tttttgtgtg aaaaagacta agagcatctt caacagtgcc 60
atgcaagaga tggaggttta cgtggagaac atccgcagaa gtttggggtt ttttaattact 120
ctccatttag gacaccctac acaccaaca gccagtatca aatgctgctc gatcccacca 180
accccgagcg cggcactgcc aagatagaca agcaggagaa ggtcaagctc aactttgaca 240
tgacggcatc ccccaagatc ctgatgagca agcctgtgct gagtgggggc acaggccgcc 300
ggatttcctt gtcggatatg ccgcgctccc ccagtagcac aaactcttct gtgcacacgg 360
gctccgacgt ggagcaggat gctgagaaga aggccacgtc gagccacttc agtgcgagcg 420
aggagtccat ggacttccag ggataagagc acagcttcac cagccatcca ccaagacggg 480
acaagcaggg agtttatccg gcagcccaaa gcccttctct cctcaactgt cagctcctat 540
cacgacgaaa acggacaaaa cctccaccac cggcagcatc ctgaatctta acctggatcg 600
aagcaaagct gagatggatt tgaaggagct gagcgagtcg gtccagcaac agtcaccccc 660
tgttcctctc atctctccca agcgccagat tcgtagcagg ttccagctga atcttgacaa 720
gaccatagag agttgcaaa cacaattagg cataaatgaa atctcggaag atgtctatac 780
ggccgtagag cacagcgatt cggaggattc tgagaagtca gatagtagcg atagttagta 840
tatcagtgat gatgagcaga agtctaagaa cgagccagaa gacacagagg acaaagaagg 900
ttgtcagatg gacaaagagc catctgtgtt taaaaaaaag cccaagccta caaacccagt 960
ggagattaaa gaggagctga aaagcacgtc accagccagc gagaaggcag accctggagc 1020
agtcaaggac aaggccagcc ctgagcctga gaaggacttt tccgaaaagg caaaccttct 1080
acctcaccoc ataaaggata aactgaaggg aaaagatgag acggattccc caacagtcca 1140
tttgggcctg gactctgatt cagagagcga acttgtcata gatttaggag aagaccattc 1200
tgggcgggag ggtcgaaaaa ataagaagga acccaaagaa ccatctccca aacaggatgt 1260
tgtaggtaaa actccaccat ccacgacggt gggcagccat tctcccccg aaacaccggt 1320
gctcaccgcg tcttccgccc aaacttcgcg ggctggcgcc acagccacca ccagcacgtc 1380
ctccacggtc accgtcacgg ccccgcccc cgccgccaca ggaagcccag tgaaaaagca 1440
gaggccgctt ttaccgaagg aggaactgcc cgcccggtga gcgggtccgt gtggaactca 1500
tcaagtaaaag tttcaaactg cct
1523

```

## (2) INFORMATION ON SEQ ID NO. 133:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2241 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

006739E-12700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

cgccgccc aa ggcgcaga ag ccgagctggg aaaagggagg cagaggaggc ggaggcagag 60
gcagaggcag agcccgggtgc cgagaccaag cgacagaccg gcgggggctgg gcctcgcaaa 120
gccggctcgg cgagctctcc cgacacccga gccggggagg aaaagcagcg actcctcgct 180
cgcatccccg ggagccgcac tccagactgg cccggtagtc aggggctcag gagcagatcc 240
cgaggcaggc tttgctcagc ctccgacgag ggctggccct ttggaaggcg ccttcaacag 300
ccggaccaga caggccacca tgaccgagaa ttccacgtcc gccctgctgg ccaagcccaa 360
gcggggccaa gcctccaaga agtccacaga ccaccccaag tattcagaca tgatcgtggc 420
tgccatccag gccgagaaga accgcgctgg ctctcgcgc cagtccattc agaagtatat 480
caagagccac tacaagggtgg gtgagaacgc tgactcgag atcaagttgt ccatcaagcg 540
cctggtcacc accggtgtcc tcaagcagac caaaggggtg ggggcctcgg ggctcctccg 600
gctagccaa agcgacgaac ccaagaagtc agtggccttc aagaagacca agaaggaaat 660
caagaaggta gccacgccaa agaaggcatc caagcccaag aaggctgcct ccaaagcccc 720
aaccaagaaa cccaaagcca ccccggtcaa gaaggccaag aagaagctgg ctgccacgcc 780
caagaaagcc aaaaaaccca agactgtcaa agccaagccg gtcaaggcat ccaagcccaa 840
aaaggccaaa ccagtgaaac ccaaagcaaa gtccagtgcc aagagggccg gcaagaagaa 900
gtgacaatga agtcttttct tgcggacact ccctcctgtc tcctattttc tgtaaataat 960
tttctccttt tttctctctt gatgtcacc accacctttt gcccccttct gttctgactt 1020
tataagagac aggatattga ttcttcagaa attacagaat aattcatttt tccttaacca 1080
gttgtgcaag gacagcaaca accaatctaa tgatgagaat gtacttatat tttgttttgc 1140
tattaaccta cttacgggggt tagggatttg cgggggggct tgtgtgtttt gttggcttgt 1200
ttgccatgaa ggtagatgtg ggtggggaga agacacaagg cagtttgttc tggctagatg 1260
agaggggaacc caggaattgt gaggttagca ggaatatctt tagggtgagt gagttttcct 1320
tgagttgggg acccgttgtg agagtttcag aacctttggc cagcaggaga gaggtggtag 1380
ggagcagcca gccggcaaa ggaaggagtg gaaaaaaacc gccaccgggc tgacttcac 1440
ctcccagtg tgagcagtg gggcccaaac ccagtttct tctcattttt gttagtttgc 1500
cctttcggcc tccctatttt cttagggaag gggagtgggg tccaagtgc agctggatgg 1560
gagaagccat agtttctccc agtcagctag gatgtagcca ttgggggatc tttgtggctt 1620
cagcaaattc tcttgtaaaa ccgagtgaa aacttcaggg gaaggggtgg gagtcagcca 1680
agtgcctcag tgtgccctgt tgaaacttag gtttttccac gcaatcgatg gatttgttcc 1740
taggaagact tttcttttcc tctggatttt tgttctctct gtacaagagg tgtctttgct 1800
tggtttggtg gggctgcggc cacttaaaac ctcccgatct ctttttgagt cctttattat 1860
aagtagttgt agctgcggga gggggagggg gagtgggagg gcagtggata gtaagactta 1920
ctgcagtcga tttgggattt gctaagtagt ttacagagc tagatctgtg tgcagtgtgt 1980
tgtttgtgta tatatacata tctagggtta gtacttagtt tcacaccggg gagctgggag 2040
aaaaaacctg tacagttgtc tttctcttat ttttaataaa atagaaaaat cgcgcacttg 2100
cgcgctcccc cccaccccc ttttttaaac aagtgttact tgtgccggga aaattttgct 2160
gtctttgtaa ttttaaaact ttaaaataaa ttggaaaagg gagaaaactga aaaaaaaaaa 2220
aaaaaaaaaa a a 2241

```

002227 5552950

## (2) INFORMATION ON SEQ ID NO. 134:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 631 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```

tgacaatggc ttcttttaaaa tactcagagg acaggatcac ggtggaatcg aatcagaagt 60
ggtggctgga attccacgca ccgatcagta ctgggaaaag atctaactcg ccgtgggcct120
gtcgtgccag tcctgggggc gagatggggg tagaaatgca tgtgatgcgt taagttcacg180
taagatacaa gtttcagaca gggtcggaag gactggattg gccaaacatc agacctgtct240
tccaaggaga ccaagtcctg gctacatccc agcctgtggt tacagtgcag acaggccatg300
tgagccaccg ctgccagcac agagcgtcct tccccctccg tgatccatcc atctccaggg360
agcaagacag agacgcagga atggaaaagcg gaggttcctaa caggatgaaa gttcccccat420
cagttccccc agtacctcca agcaagtagc tttccacatt tgtcacagaa atcagaggag480
agatggtggt gggagccctt tggagaacgc cagtctccca ggccccctgc atctatcgag540
tttgcaatgt caaacctctc tgatcttgtg tcagatgatt cttaatagga gtttatcttt600
cgggcagctg cgaatcaggg gggtaaccag g

```

## (2) INFORMATION ON SEQ ID NO. 135:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 980 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

09673396-122700



## (vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```

ggggccggga ggggtacttag ggccggggct ggcccaggct acggcggctg cagggctccg 60
gcaaccgctc cggcaacgcc aaccgctccg ctgcgcgcag gctgggctgc aggctctcgg120
ctgcagcgct ggggtgatct aggatccggc ttccaacatg tggcagctct gggcctccct180
ctgctgcctg ctggtgttg ccaatgcccg gagcaggccc tctttccatc ccctgtcgga240
tgagctggtc aactatgtca acaaacggaa taccacgtgg caggccgggc acaacttcta300
caacgtggac atgagctact tgaagaggct atgtggtacc ttcctgggtg ggcccaagcc360

accccagaga gttatgttta ccgaggacct gaagctgcct gcaagcttcg atgcacggga420
acaatggcca cagtgtccca ccatcaaaga gatcagagac cagggctcct gtggctcctg480
ctgggccttc ggggctgtgg aagccatctc tgaccggatc tgcattccaca ccaatgcgca540
cgtcagcgctg gaggtgtcgg cggaggacct gctcacctgc tgtggcagca tgtgtgggga600
cggctgtaat ggtggctatc ctgctgaagc ttggaacttc tggacaagaa aaggcctggt660
ttctgggtggc ctctatgaat cccatgtagg gtgcagaccg tactccatcc ctccctgtga720
gcaccacgtc aacggctccc ggcccccatg cacgggggag ggagataccc ccaagtgtag780
caagatctgt gagcctgggt acagcccagc ctacaaacag gacaagcact acggatacaa840
ttctacagcg tctccaatag cgagaaggac atcatggccg agatctacaa aaacggcccc900
gtggagggag gttctctgtg tattcggact tctgcctaga gtcagggggg acaaaaagtcc960
cgggaatttg gggggccgcc
980

```

## (2) INFORMATION ON SEQ ID NO. 136:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2238 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

0967339E-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```

cacatgttcg gggaccgagt ggggtcaatc ttctgggtgct gcctctccag gtctcttcca 60
ggccgggcat agacgtactc cctctgaggc cgaccgatgg ttagaagagg tgtctaagag 120
cgctccgggt cagcagcccc aggcctcagc tgctcctctg cagccagttc tccagcctcc 180
tccacccact gccatctccc agccagcacc acctttccaa gggaatgcac tcctcacctc 240
tcagcctgtg ccagtgggtg tggccccagc cctgcaacca gcctttgtcc ctgcccagtc 300
ctatcctgtg gccaatggaa tgccctatcc agcccctaata gtgcctgtgg tgggcatcac 360
tccctcccag atggtggcca acgtatattg cactgcaggc caccctcagg ctgcccaccc 420
ccatcagtc aacagcctgg tcaggcagca gacattccct cactacgagg caagcagtcg 480
taccaccagt cctttcttta agcctcctgc tcagcacctc aacgggttctg cagctttcaa 540
tggtgtagat gatggcaggg tggcctcagc agacaggcat acagagggtc ctacaggcac 600
ctgcccagtg gatccttttg aagcccagtg ggctgcatta gaaaataagt ccaagcagcg 660
tactaatccc tccctacca accctttctc cagtgcattc cagaagacgt ttgaaattga 720
actttaagca atcattatgg ctatgtatct tgtccatacc agacaggagg cagggggtag 780
cggtcaaagg agcaaaacag actttgtctc ctgattagta ctcttttcac taatcccaaa 840
gggtcccagg aacaagtcca ggcccagagt actgtgaggg gtgattttga aagacatggg 900
aaaaagcatt cctagagaaa agctgccttg caattaggct aaagaagtca aggaaatgtt 960
gctttctgta ctccctcttc ccttaccccc ttacaaatct ctggcaacag agaggcaaaag 1020
tatctgaaca agaattctata ttccaagcac atttactgaa atgtaaaaca caacaggaag 1080
caaagcaatc tccctttgtt ttccaggcca ttccctgccc tcctgtcagt agtggcctgt 1140
attagagatc aagaagagtg gtttgtgctc aggtggggga acagagaggc acgctatgct 1200

gccagaattc ccaggagggc atatcagcaa ctgcccagca gagctatatt ttgggggaga 1260
agttgagctt ccattttgag taacagaata aatattatat atatcaaaag ccaaaatctt 1320
tatttttatg catttagaat attttaataa gttctcagat attaagaagt tgtatgagtt 1380
gtaagtaatc ttgccaaagg taaaggggct agttgtaaga aattgtacat aagattgatt 1440
tatcattgat gcctactgaa ataaaaagag gaaaggctgg aagctgcaga caggatccct 1500
agcttgtttt ctgtcagtca ttcatgttaa gtagcacatt gcaacaacaa tcatgcttat 1560
gaccaataca gtcactaggt tgtagttttt tttaaataaa ggaaaagcag tattgtcctg 1620
gttttaaaacc tatgatggaa ttctaattgc attattttta tggaaatcaat cgaaatatgc 1680
tctatagaga atatatcttt tatatatgct tgcagtttcc ttatgttaat cctttaacac 1740
taaggtaaca tgacataatc ataccataga agggaaacaca ggttaccata ttgggtttgt 1800
atatgggtct tgggtgggtt tgttttatcc tttaaatttt gttcccatga gttttgtggg 1860
gatggggatt ctggttttat tagctttgtg tgtgtcctct tccccaaaac ccccttttgg 1920
tgagaacatc cccttgacag ttgcagcctc ttgacctcgg ataacaataa gagagctcat 1980
ctcattttta cttttgaacg ttggccttac aatcaaattg aagttatata tattgtact 2040
gatgaaaatt tataatctgc ttttaacaaa ataaatgttc atggtagaaa aatttgccca 2100
tgaagggtcg ttctttcccc tttcctttat tagtaaatga atttattttt cgttcttttg 2160
gtcttactct ccattctact gctgctgtaa atccctagtt tagtgactag aaaaataccc 2220
ttaagattca tattttca
2238

```

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 137:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 398 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```
tgcagattgg ttgggggcagc cccggggaggc tggctccgac acacgactga gtgtgcctac 60
actggtccca caggttttca gctgtggagt ttgggatctg agcttggagc ccatttggtt120
ctggcagttc cgctcatatt ttccacttga agacatcgcc tccgttcctt ccaagctggg180
agaccagaag tcaacaacag gaggggtggag aggccgggtc tcacaatccg cttggctggg240
gagtccactg aggttcttgc atcctgaagc aaaccatgga gagctgggtg ggacttccct300
gttttgcggt cctgtgtttt ctaatgcacg cccgagggtca aagagacttt gattttggca360
gatgcccttg atgaccctga aaccaccaa gaagccaa 398
```

## (2) INFORMATION ON SEQ ID NO. 138:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1084 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

09673395.122700

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

ggcgggtggcg gaagtgggag cgggcctgga gtcttggcca taaagcctga ggcggcgggca 60
cggcgaggatt ggcggcttgg agagctcggg agagttccct ggaaccagaa cttggacctt 120
ctcgtttctg tcctccgttt agtctcctcc tcggcgggag cctcgcgacg gcccgggccg 180
gagccccag cgcaggcccc cgtttgaagg atgacctcta ggaagaaagt gttgctgaag 240
gttatcatcc tgggagattc tggagtcggg aagacatcac tcatgaacca gtatgtgaat 300
aagaaattca gcaatcagta caaagccaca ataggagctg actttctgac caaggaggtg 360
atggtggatg acaggctagt cacaatgcag atatgggaca cagcaggaca ggaacggttc 420
cagtctctcg gtgtggcctt ctacagaggt gcagactgct gcgttctggt atttgatgtg 480
actgccccca acacattcaa aaccctagat agctggagag atgagtttct catccaggcc 540
agtccccgag atcctgaaaa cttcccatth gttgtgttgg gaaacaagat tgacctcgaa 600
aacagacaag tggccacaaa gcgggcacag gcctggtgct acagcaaaaa caacattccc 660
tactttgaga ccagtgccaa ggaggccatc aacgtggagc aggcgttcca gacgattgca 720
cggaatgcac ttaagcagga aacggaggtg gagctgtaca acgaatttcc tgaacctatc 780
aaactggaca agaatgaccg ggccaaggcc tcggcagaaa gctgcagttg ctgagggggc 840
agtgaagatt gagcacagag tccttcacaa accaagaaca cacgtaggcc ttcaacacaa 900
ttccctctc ctcttccaaa caaaacatac attgatctct cacatccagc tgccaaaaga 960
aaaccccatc aaacacagtt acaccccaca tattctctca cacacacaca cacacggcac 1020
acacacacac acaggtttgg acgttattca gattgcggcc tttgccgtgt tgggttcgtg 1080
gggg

```

(2) INFORMATION ON SEQ ID NO. 139:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1259 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

004221 56E/960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

taaaatacag aagaagagtc cacacactgt ttcacgagaa ggagtgtatc atgattttgta 60
gtaatcgaag aacatgttta tgggaacagg gtgactcagc tctcctgggg aggatggatg 120
aggagtttagc aggaagagag ggtaccaagt gaggggaaag cagcaggggtg ggtctggggc 180
atggacagga agcagaggct gggaaaagct acatctttta ttcattgcttt ttcacaggag 240
ctgaagtggg aatcagtaga tcgagaatcc acggccgggg accagtagga cttgagggac 300
tgcttactac taagtggctg ctgagaggga aggaccacgt ggtctcagat ttctcagagc 360
atggaagttt aaaatatctt catgagaacc tccctattcc tcagagaaac accaactgaa 420
aagagccagg aaaacccggg aattttccaa aaggctctca cgttaaactt gtcttatctc 480
aggagagagc ccgctcttgt ctcccagttc ctggtagggg ctgcctgttg gaaagtgtac 540
ctggatgctt ctgggctccg tttggcaata gcaatcttgg ctgatgtgca cagtctggct 600
cccagctcac cctttttttt taaaagtaag aaaatagttg ctaccgatag ggacttggcc 660
aagtccaatt atcttctagg attgaaaggt gcattttccc cataaaaaag gcgaggaa 720
cccatggctg ctttgtgtca cctcagtga cttacagtc ccttggcatt tagttggtag 780
tagagccagt catccttaac aaatcttttc acattttatt tctttcacat gtagtcatct 840
tcaaaaagga aagatttgga atttttagaa aggggcaact cttcttttta gcattctcat 900
cagaaagtca caaaaatcga tggaatcatt tccactggga agattgacct tttgtattta 960
tttgtggggt aaattaataa gcattccaga tgcttcagc ttcttcgcat caggagatgc 1020
tgtgttcccc gtgatgcagc tggaacccaa gctgcagcag gagatgcaag tttcaggatg 1080
ttccccactg agctggagga atatctacag cagtgatgct tgaaattttt gtatgaattt 1140
ttttgtcgtc ctaccctttt cctccaaaac aaaaattaga ggattatttt aatactttgg 1200
attcttcccc cttttttgag aaataaagtt ttttatgaaa agccaaaaaa aaaaaaaaaa 1259

```

## (2) INFORMATION ON SEQ ID NO. 140:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1938 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004221" 56E4960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

ccaagatggc ggcacgatgc ctgcccggct gttgggggtgg cggtgacgac aggcagcaaa 60
agaccagctg gtcccagatt cgctgctgga gtgctggatg gagcctttct ctgccctctg 120
tgacatttcc aatttttagat aatgcctcac atctctgtcc ccccgggacc ccctggagcc 180
cccatgatcc ctaagaagac agcttgaacc tagatctcac ccccaggatg ttgcgaggcc 240
tgctggagcg gccttgacag ctggccctgc ttgtgggctc ccagctggct gtcattgatgt 300
acctgtcact ggggggcttc cgaagtctca gtgccctatt tggccgagat cagggaccga 360
catttgacta ttctcaccct cgtgatgtct acagtaacct cagtcacctg cctggggccc 420
cagggggctc tccagctcct caaggctctgc cctactgtcc agaacgatct cctctcttag 480
tgggtcctgt gtccgtgtcc tttagcccag tgccatcact ggcagagatt gtggagcgga 540
atccccgggt agaaccaggg ggcgggtacc gccctgcagg ttgtgagccc cgctcccga 600
cagccatcat tgtgcctcat cgtgcccggg agcaccacct gcgcctgctg ctctaccacc 660
tgacccctt cttgcagcgc cagcagcttg cttatggcat ctatgtcatc caccaggctg 720
gaaatggaac atttaacagg gcaaaaactgt tgaacgttgg ggtgcgagag gccctgcgtg 780
atgaagagtg ggactgcctg ttcttgacag atgtggacct cttgccagaa aatgaccaca 840
atctgtatgt gtgtgacccc cggggacccc gccatgttgc cgttgctatg aacaagttt 900
gatacagcct cccgtacccc cagtacttct gaggagtctc agcacttact cctgaccagt 960
acctgaagat gaatggcttc cccaatgaat actggggctg ggggtggtag gatgacgaca 1020
ttgctaccag ggtgcgcctg gctgggatga agatctctctg gccccccaca tctgtaggac 1080
actataagat ggtgaagcac cgaggagata agggcaatga ggaaaatccc cacagatttg 1140
acctcctggc ccgtacccag aattcctgga cgcaagatgg gatgaactca ctgacatacc 1200
agttgctggc tcgagagctg gggcctcttt ataccaacat cacagcagac attgggactg 1260
accctcgggg tcctcgggct ccttctgggc cacgttacct acctggttcc tcccaagcct 1320
tccgtcaaga gatgctgcaa cgccggcccc cagccaggcc tgggcctcta tctactgcca 1380
accacacagc cctccgaggt tcacactgac tcctccttcc tgtctacctt aatcatgaaa 1440
ccgaattcat ggggttgtat tctccccacc ctgagctcct cactgttctc agagggatgt 1500
gagggaaactg aactctggtg ccgtgctagg gggtaggggc ctctccctca ctgctggact 1560
ggagctgggc tcctgtagac ctgaggggtc cctctctcta gggctcctg tagggcttat 1620
gactgtgaat ccttgatgtc atgattttat gtgacgattc ctaggagtcc ctgcccctag 1680
agtaggagca gggctggacc ccaagcccct cctcttcca tggagagaag agtgatctgg 1740
cttctcctcg gacctctgtg aatattttat ctattttatg ttcccgggaa gttgtttggt 1800
gaaggaagcc cctccctggg cattttctgc ctatgctgga atagctccct cttctgggtc 1860
tggctcaggg ggctgggatt ttgatatttt ttctaataaa ggactttgtc tcgcaaaaaa 1920
aaaaaaaaa aaaaaaaaaa 1938

```

## (2) INFORMATION ON SEQ ID NO. 141:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1874 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

004221" 56EE2960

## (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```

caaaaaaacc tcttaatat ctggagtcac cattcccttc gacagcattt tectctgctt 60
tgaaagcccc agaaatcagt gttggccatg atgacaacta cagaaaaaacc agaggcagct 120
tctttgccaa gacctttcaa agccatttta ggctgttagg ggcagtggag gtagaatgac 180
tctttgggta ttagagtttc aaccatgaag tctctaacaa tgtattttct tcacctctgc 240
tactcaagta gcatttactg tgtctttggt ttgtgctagg cccccgggtg tgaagcacag 300
accccttcca ggggtttaca gtctatttga gactcctcag ttcttgccac tttttttttt 360
aatctccacc agtcattttt cagacctttt aactcctcaa ttccaacact gatttccctt 420
tttgcaattct cctccttcc ctctcttgta gccttttgac tttcattgga aattaggtatg 480
taaactctgct caggagacct ggaggagcag aggataatta gcatctcagg ttaagtgtga 540
gtaactctgag aaacaatgac taattcttgc atattttgta acttccatgt gagggttttc 600
agcattgata tttgtgcatt ttctaaacag agatgagggt gtatcttcac gtagaacatt 660
ggatttcgct tgagaaaaaa agaatagttg aacctatttc tctttcttta caagatgggt 720
ccaggattcc tcttttctct gccataaatg attaatataa tagcttttgt gtcttacatt 780
ggtagccagc cagccaaggc tctgtttatg cttttggggg gcatatattg gggtccattc 840
tcacctatcc acacaacata tccgtatata tcccccttac tcttacttcc cccaaattta 900
aagaagtatg ggaaatgaga ggcatttccc ccacccatt tctctcctca cacacagact 960
catattactg gtaggaactt gagaacttta tttccaagtt gttcaaacat ttaccaatca 1020
tattaataca atgatgctat ttgcaattcc tgctcctagg ggaggggaga taagaaaccc 1080
tcactctcta caggtttggg tacaagtggc aacctgcttc catggccgtg tagaagcatg 1140
gtgcccctggc ttctctgagg aagctggggg tcatgacaat ggcagatgta aagttattct 1200
tgaagtccag ttgaggctgg gagacagccg tagtagatgt tctactttgt tctgctgttc 1260
tctagaaaga atatttggtt ttctgtata ggaatgagat taattccttt ccagggtatt 1320
tataattctg ggaagcaaaa cccatgcctc cccctagcca tttttactgt tatcctattt 1380
agatggccat gaagaggatg ctgtgaaatt cccaacaaac attgatgctg acagtcatgc 1440
agtctgggag tggggaagtg atcttttggt cccatcctct tcttttagca gtaaaatagc 1500
tgagggaaaaa gggagggaaa aggaagttaa gggaatacct gtgggtggtg tgatccctag 1560
gtcttgggag ctcttggagg tgtctgtatc agtggaattc ccatccctg tgggaaatt 1620
gtaggctcat ttactgtttt aggtctagcc tatgtggatt ttttcctaac atacctaaagc 1680
aaaccacagt tcaggatggg aattcttatt ctttcgttca gtttaagttt tcccttcatt 1740
tgggcactga agggatatgt gaaacaatgt taacattttt ggtagtcttc aaccagggat 1800
tgtttctgtt taacttctta taggaaagct tgagtaaaat aaatattgtc tttttgtatg 1860
tcaaaaaaaaa aaat

```

004221 55864960

## (2) INFORMATION ON SEQ ID NO. 142:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 198 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

004227 5555/950  
RDIWTMNLQR YWGEIPISSS QTNRSSFDLL PREFRLVEVH DPPLHQPSAN KPKPPTMLDI 60  
PSEPCSLTIH TIQLIQHNRR LRNLIATAQA QNQQQTGKVK TEESEPLPSC PGSPPLPDDL120  
LPLDCKNPNA PFQIRHSDPE SDFYRGKGEP VTELSWHSCR QLLYQSGGTN PGQRRAFDCA180  
NESVLEDPNL MLAHEYWP 198

## (2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 92 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

IVWMVRLHGS EGMSSIVGGF GLLAEGWCRG GSWTSTRNS RGSKSKELLL VWLDDIGISP60  
QYLCRFIVHM SLQVQQTFIK CQAFCVGQRL IM 92

## (2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 96 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

DPCPERSTKN RHGAQGMFKS LQGFPRSRSA GAGANHRVLR SPDVQGSRTK GRSGPEPRQG60  
GTTLFTAASQ SGLGGCLDLE RPEARIASDP ESWFVD 96

(2) INFORMATION ON SEQ ID NO. 145:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 52 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

EGRVQQGSFV NVQQGPQEPF IEFHQLTQA IKSTHGTSTI PRVSRITLKD KP 52

(2) INFORMATION ON SEQ ID NO. 146:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 47 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

PSRTSHSGTL PIPRLKICFK KRGNMNKDPT TLLAQVLFTL NFLNLDN

47

00/22/95 12:22:00

## (2) INFORMATION ON SEQ ID NO. 147:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

LSKFKKLRVN NTCASSVVGS LFIFPLFLKH IFKRGMGVNP LWLVLEGYTR YPWNGRCSMC60  
 ALNCLG 66

## (2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 187 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

REGEGRPEGN GDIRGGLRSG CDLSLLAPLL PPSSSESWE CYPWKIKLGL QELSVWEESM 60  
 AQHSACVPFC SGSLSPPPSQ PQLSPSPSS SPEDSSDGRA GPPEPTGSSG CTGSWCSLSP120  
 VHFHSHWMEC PCILCCRSPH LHLRGLGSPS SPQCPQSLSQ TVGWNMRLEA ERGSEHHSPC180  
 TWVASCP 187

00/222T"56EE/960

## (2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 147 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

REDWNRGKGE VAPCFVQPGS WQPCWGLDP TTPAHLAEHL VPIEDCLPLL LHLQLPPLL 60  
TFHTLQDCVC SGSPGECSSC CHRASILLL LIVQLLSVCI RLSDQRVHQH QEGHVEQQGT120  
HHGQVDDNDD LDGGGLRSSY LSHSRQ 147

## (2) INFORMATION ON SEQ ID NO. 150:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 142 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

FFFFFFWREIK QFNDGFLLDH TTLRQEDKIF SPCTGTTKFR DKRQPKYRGC GVQIHAQPRV 60  
SCSNRPSGSV TVDTGERRDC PDPSSAGEGT GSRVCMGTPC PSARSAQGTA NTSFQCTLKT120  
QWAQGAQLSH QSCPQGWSWG WG 142

## (2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 464 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

00422T 55557950

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```

RQOTVLGSCS SSILPCQLLK HQGSSKTEMT KNWLIQTKRR YFSSPKQMSM THWPRTAWLT 60
GCSVTLFLFP SQYVDVASLG LVPQLTGGTL YKYNFMQHL DRQQFLNDLR NDIEKKIGFD120
AIMRVRTSTG FRATOFFGGI LMNNTTDVEM AAIDCDKAVT VEFKHDDKLS EDSGALIQCA180
VLYTTISGQR RLRIHNLGLN CSSQLADLYK SCETDALINF FAKSAFKAVL HQPLKVIREI240
LVNQTAHMLA CYRKNCASPS AASQLILPDS MKVLPVYMNC LLKNCVLLSR PEISTDERAY300
QRQLVMTMGV ADSQLFFYPQ LLPIHTLDVK STMLPAAVRC SESRLSEEGI FLLANGLHMF360
LWLGVSPPPE LIQGIFNVPS FAHINTDMTL LPEVGNPYSQ QLRMIMGIIQ QKRPYSMKLT420
IVKQREQPEM VERQFLVEDK GLYGGSSYVD FLCCVHKEIC QLLN 464

```

(2) INFORMATION ON SEQ ID NO. 152:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 172 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```

TMLEKIPKEE QEETSAIRVG FITYNKVLHF FNVKSNLAQP QMMGVTDVGE VEVPLLDGFL 60
VNYQESQSVI HNLLDQIPDM FADSNENETV FAPVIQAGME ALKAADCPGK LFIFHSSLPT120
AEAPGKLKNR DDKKLVTNDK EKILFQPQTN VYDSLAKDCV AHRLLCOTLP LS 172

```

(2) INFORMATION ON SEQ ID NO. 153:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 141 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

004221 56E/960

(vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

141

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

LDRCGLYPVS	SLLQVEGSLW	RAAGVFQPPP	GLAHANDWRF	TARVHGGALG	EHDKMVAAAT 60
GSEILLWALQ	AEGGGSEIGV	FHLGVPVEAL	FFVGNQLIAT	SHTGRIGVWN	AVTKHWQVQE120
VQPKITSYDAA	GSFLLLGCSN	GSIIYYVDVQK	FPLRMKDNDL	LVSELYRDPA	EDGVTALSVY180
LTPKTSYDSGN	WIEIIAYGTSS	GGVRVIVQHP	ETVGGSGPQLF	QTFTVHRSPV	TKIMLSEKHL240
ISVCADNNHV	TRWSVTRFRG	MISTQPGSTP	LASEKILALE	SADGHGCGSA	GNDIGPYGER300
DDQQVFIQKV	VPSASQLFVR	LSSTGQRVCS	VRSVDGSPTT	AFTVLECEGS	RRLGSPRRY360

```

LLTGQANGSL  AMWDLTTAMD  GLGQAPAGGL  TEQELMEQLE  HCELAPPAPS  APSWGCLPSP420
SPRISLTS LH  SASSNTSLSG  HRGSPSPQA  EARRRGGGSF  VERCQELVRS  GPDLRRPPTP480
APWPSSGLGT  PLTPPKMKLN  ETSF

```

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 289 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

(2) INFORMATION ON SEQ ID NO. 156:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

(2) INFORMATION ON SEQ ID NO. 157:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

QLWGFAAGSD SRPAMGCDGG TIPKRHELVK GPKKVEKVDK DAELVAQWNY CTLSQEILRR 60  
 PIVACELGRL YNKDAVIEFL LDKSAEKALG KAASHIKSIK NVTELKLSN PAWEGDKGNT120  
 KGDKHDDLQR ARFICPVVGL EMNGRHRFCF LRCCGCVFSE RALKEIKAEV CHTCGAAFQE180  
 DDVIVLNGTK EDVDVLKTRM EERRLRANWK RKQRNPRQQS LFQNMMSVKK PQGHQKLRQG240  
 SLKKPALILE RRPPTWLPKA QQ 262

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 138 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

CHRAQWHQGG CGRAEDKDGG EKAESELEKK TKKPKAAESV SKPDVSEEAP GPSKVKTGKP 60  
 EEASLDSREK KTNLAPKSTA MNESSSGKAG KPPCGATKRS IADSEESEAY KSLFTTHSSA120  
 KRSKEESAHW VTHTSYCF 138

(2) INFORMATION ON SEQ ID NO. 159:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 168 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

HLVLKQTLTP WVSLSFSPIR SQPSLLHPCL QHVHILLGAI EHDDIILLEG SPTRVANFRF 60  
 YLFQGSRLKH TAAAPKEAEP VSAVHLQAHN GADETRPLEV IVLVTFVSVE IPFPGRIRK120  
 LQLCHILNAF NVRCCLPKSL FCRFVQEKFN DGIFVIKSAK FTGNYWSS 168

(2) INFORMATION ON SEQ ID NO. 160:

000222" 5622950

- |            |            |            |            |            |               |     |
|------------|------------|------------|------------|------------|---------------|-----|
| HQWHITAMGS | QHSAAARPSS | CRRKQEDDRD | GLLAEREQEE | AIAQFPYVEF | TGRDSITCLT    | 60  |
| CQGTGYIPTE | QVNELVALIP | HSDQRLRPQR | TKQYVLLSIL | LCLLASGLVV | FFLPHSVLV120  |     |
| DDDGIKVVKV | TFNKQDSLVI | LTIMATLKIR | NSNFYTVAVT | SLSSQIQYMN | TVVNFTGKAE180 |     |
| MGGPFSYVYF | FCTVPEILVH | NIVIFMRTSV | KISYIGLMTQ | SSLETHHYVD | CGGNSTAI      | 238 |

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 91 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN
      (A) ORGANISM: HUMAN
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

SSHEOHYVVH QDLRYAAEEV HIGKRSSH LG LPGKIHHCVH VLNLAQAGH CHRVEVGVDPD60  
FQGGHDGENY KGVLLIKCDF HHFDAVIIHK D 91



## (2) INFORMATION ON SEQ ID NO. 162:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 133 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

MRKQEENHQT RCQETKQDGQ EDILLSSLRA QSLITVWDQS HQLIYLLCWN VACPLARETG 60  
 DAISPGEFHI WELSNQFFLL SFSQQTVPVI FLLSPAGGGA SSSGMLRPHG RDMPLVSCPA120  
 SSVGGAARTQ RAG 133

## (2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

AAGAAGPHRR RHPLHPSLLR EHHSQAQAPG GVRPGQSTLS RIEAVQPQLP RPSGLPSLWG60  
 WLPWLLGTRP QRHPEIPPET QCASTAVRRS A 91

## (2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 174 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00673395-122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

LDNPTQRNKD QLIRAAVKFL DTDTCYRVE EPETLVELQR NEWDPPIEWA EKRYGVEISS 60  
 STSIMGPSIP AKTREVLVSH LASYNTWALQ GIEFVAAQLK SMVLTGLID LRLTVEQAVL120  
 LSRLEEEYQI QKWGNIEWAH DYELQELRAR TAAGTLFIHL CSESTTVKHK LLKE 174

(2) INFORMATION ON SEQ ID NO. 165:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 66 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CLGLLHPVAD GVGVQKLHGC PDQLILVSLG WVVQSRVAQC GQVHGVVLDG ILLGIPLSTL60  
 CTCQGL 66

(2) INFORMATION ON SEQ ID NO. 166:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 132 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

SWRETEIKEQ LTHELCTIIQ QNELRKAKKL EELMQQLDVE ADEETLELEV EVERLLHEQE 60  
 VESRRPVVRL ERPFQPAEES VTLEFAKENR KCQEQAQVSPK VDDQCGNSSS IPFLSPNCPN120  
 QEGNDISAAL AT 132

004227" 56527960

## (2) INFORMATION ON SEQ ID NO. 167:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 67 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

QILMSHSPPQ AEMASLNEPL VSLILLVVRV AISRPPQAP KSLHRLHLV VASTPPTSWP60  
FGAHFAV 67

## (2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 74 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

NGLSKRTTGL LDSTSCSCSN LSTSTSSSKV SSSASTSSCC INSSNFLAFR SSFCCMIVQR60  
CSVSCSFISV SRHE 74

## (2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 89 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

002221" 56E/960

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

GRGGLGCRSW RCAGSSRPYS EVFSVALLER GSSCILRIFC ISAPFSSRCH RMPQIGPVPS60  
VNQTSETASL QGQSPSTDEL ERDSEMQRP 89

(2) INFORMATION ON SEQ ID NO. 170:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 74 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

GPLHFRIPLK LICTWTTLTK RGGFRSLIHR GDRTYLGHPM AARREGSRNA KYSQDAGGTP60  
LKERHGENFR VRAR 74

(2) INFORMATION ON SEQ ID NO. 171:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 89 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

AVAFQNPSQA HLYLSDPEA RRFPKSDSPR GQDLFGASDG SEKRREPKCK IFSRCRRNPS60  
QGAPRRKLQS TGAMIQHNAR TCSPAHLSP 89

002227" 56E2960

## (2) INFORMATION ON SEQ ID NO. 172:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 100 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

PSPAVLGDQP PSASGAVHRK LSLEVCCCQE RAQMGPVMAA TSTSCGRARL LARSAQWLTT 60  
 MLSSAAVWLG SRRLTTCGEN PSYALVAFLC LSRESPSAKP 100

## (2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 495 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

SRTNTPVETW KGSKGKQSYT YIIIEENTTTS FTWAFQRTTF HEASRKYTND VAKIYSINVT 60  
 NVMNGVASYC RPCALEASDV GSSCTSCPAG YYIDRDSGTC HSCPPNTILK AHQPYGVQAC120  
 VPCGPGTKNN KIHSLCYND CTFSRNTPTRT FNYNFSALAN TVTLAGGPSF TSKGLKYFHH180  
 FTLSLCGNQG RKMSVCTDNV TDLRIPEGES GFSKSITAYV CQAVIIPPEV TGYKAGVSSQ240  
 PVSLADRLIG VTTDMTLDGI TSPAELFHLE SLGIPDVIFF YRSNDVTQSC SSGRSTTIRV300  
 RCSPQKTVPG SLLLPGTCS DGTCDGCNFHF LWESAAAACPL CSVADYHAIV SSCVAGIQKT360  
 TYVWREPKLC SGGISLPEQR VTICKTIDFW LKVGISAGTC TAILLTVLTC YFWKKNQKLE420  
 YKYSKLV MNA TLKDCDL PAA DSCAIMEGED VEDDLIFTSK KSLFGKIKSF TSKRTPDGFD480  
 SVPLKTSSGG PDMDL 495

## (2) INFORMATION ON SEQ ID NO. 174:

- (i) SEQUENCE CHARACTERISTIC:

00673395-122700

- (A) LENGTH: 118 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

GHNEEISSSG CCRMLAPKSP QACKGAMQGE EAGEAGSASH RMSGPPEDV FSGTESNPSG 60  
VLLEVNDLIF PKSDFLLVKM RSSSTSSPSM MAQLSAAGRS QSLRVAFITS LEYLYSSF 118

(2) INFORMATION ON SEQ ID NO. 175:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 172 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

RNTRGHFRAC QRKLKPCSVS TVYKFNRNAC QRGLFEKRVF SEPVLSVQEK GVLLKRKLSL 60  
LEQDVIVNED GRNKLKKQGE TPNEVCMFSL AYGDIPEELI DVSDFECSLC MRLFFEPVTT120  
PCGHSFCKNC LERCLDHAPY CPLCKESLKE YLADRRYCVT QLLEGINSEV SA 172

(2) INFORMATION ON SEQ ID NO. 176:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 248 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

002227 5552960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

(2) INFORMATION ON SEQ ID NO. 177:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

HSTSYLLDTL LSFLCKEDNM VHDLNNAQDN SYRTNVRKGL LLAQKTTSCR ENTRNLRHRL 60  
ILLEYHHKLR KTYRLHWEFL LVFSAYFFHL HLQSHPVLKE TTFFSAEHLF LELTEQVLRA120  
LFFQTVLSGR HFC 133

(2) INFORMATION ON SEQ ID NO. 178:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 152 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```
SAVKRGWDLN  MAAVVAATAL  KGRGARNARV  LRGILAGATA  NKASHNRTRA  LQSHSSPEGK  60
EEPEPLSPEL  EYIPRKRKGN  PMKAVGLAWA  IGFPCGILLF  ILTKREVDKD  RVKQMKARQN 120
MRLSNTGEYE  SQRFRASSQS  APSPDVGSQV  QT                                     152
```

## (2) INFORMATION ON SEQ ID NO. 179:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 114 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

EGRSAPQVCT PDPTSGDGAL WEEALNLWLS YSPVLDNRMF CRAFTCFTRS LSTSRLVRMK 60  
 RRIPOGKPMQ QASPTAFMGF LPLFLGMYSS SGDRGSGSSL PSGELWLCRA RVLL 114

## (2) INFORMATION ON SEQ ID NO. 180:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GLATAWASCA LWWTSEARTG IWAKPEDLTV NSLGGSQRSS GLHPRPNIRG RGTLLGGSPEP 60  
 LALILARVGQ PHVLPSLHLL HTVLVHFPLG EDEEEDTTRE ADGPGQSHSF HGVLAPLSGN120  
 VFQLRG 126

## (2) INFORMATION ON SEQ ID NO. 181:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

007227 5552950



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

74

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 84 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

84

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 70 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

70

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TVKFLRRLKV RGTKAGEISL SPEEGEADGS QQPALFLRVI FKFANCITGG PTFCFYQEFFF60  
FCSKTLVMGI F 71

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 55 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

YLN LQIVLQE GLLSVFIKSF SFVQRHWLWE YFERVRNAGI KRCCRLILKV LTEPV 55

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 37 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

37

## 37

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 256 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```
RSQAGPEAGQ PLPGSGKRSS CCHCSSGACS MGPLPRTVEL FYDVLSPYSW LGFEILCRYQ 60
NIWNINLQLR PSLITGIMKD SGNKPPGLLP RKGLYMANDL KLLRHHLQIP IHFPKDFLSV120
MLEKGSLSAM RFLTAVNLEH PEMLEKASRE LWMRVWSRNE DITEPQSILA AAEEKAGMSAE180
QAQGLLEKIA TPKVKNQLKE TTEAACRYGA FGLPITVAHV DGQTHMLFGS DRMELLAHLL240
GEKWMGPIPP AVNARL                                     256
```

(2) INFORMATION ON SEQ ID NO. 190:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 196 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```
SLAFTAGGIG PIHFSPSRCA SSSIRSEPNN MWVWPSTWAT VMGSPKAPYL QAASVVSLSW 60
FFTEGVAIFS RSPWACSADI PAFSAAARML CGSVMSSFLD QTRIHSSRDA FSSISGCSKF120
TAVRKRMADK LPFSSITDKK SLGKWMGIWR WCLRSFKSFA MYSPLRGSRP GGLFPLSFM180
PVMRLGRNCR LMFQIF                                     196
```

(2) INFORMATION ON SEQ ID NO. 191:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 116 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00673395-122700

EQRASAMRSS RAFRTVCSSW ATHGQLPAGL DDKTNIKTVC TYWEDFHSCT VTALTDQCQEG 60  
AKDMWDKLRK ESKNLNIQGS LFELCGSGNG AAGSLLPAFP VLLVLSAAL ATWLSF 116

(2) INFORMATION ON SEQ ID NO. 192:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 182 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

[illegible]

(2) INFORMATION ON SEQ ID NO. 193:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 105 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

HLANKTQEIK RNKKENQDFP QSYMSVFSIT ENHNVPKELM DLPLDFREHG VSVGGRAGGA 60  
GPTLRRKARS LKLPRETPGA PGTPGAGTTP PRCRCRRVRI SCLGC 105

(2) INFORMATION ON SEQ ID NO. 194:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 426 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

EIYSLSRFIE VKMSKKISGG SVVEMQGDDEM TRIIWELIKE KLIFPYVELD LHSYDLGIEN 60  
 RDATNDQVTK DAAEAIKKHN VGVKCATITP DEKRVEEFKL KQMWKSPNGT IRNILGGTVF120  
 REAIICKNIP RLVSGWVKPI IIGRHAYGDQ YRATDFVVPG PGKVEITYTP SDGTQKVTYL180  
 VHNFEEGGGV AMGMYNQDKS IEDFAHSSFQ MALSKGWPLY LSTKNTILKK YDGRFKDIFQ240  
 EIYDKQYKSQ FEAQKIWYEH RLIDDMVAQA MKSEGGFIWA CKNYDGDVQS DSVAQGYGSL300  
 GMMTSVLVCP DGKTVEAEAA HGTVTRHYRM YQKGQETSTN PIASIFAWTR GLAHRKLDN360  
 NKELAFFANA LEEVSIETIE AGFMTKDLAA CIKGLPNVQR SDYLNTEEFM DKLGENLKIK420  
 LAQAKL 426

(2) INFORMATION ON SEQ ID NO. 195:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 97 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

RLLPKHLQRR QALYCYQALL CGLTLWSRQK WKQWDWWTSP VLSGTCGSDG LQSRGQPLLL60  
 LSCHLDKPAR WSSCRESHTL GPQSPTARHH HSFYRPR 97

(2) INFORMATION ON SEQ ID NO. 196:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 93 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

00227-5667950

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

LILIIHPHGN TTTFFKVMYQ VCHLLGSVTW CVGYLYFSRP RNNKISCSVL IPISMTTYDD60  
RFYPSTHKPG DIFADNGFSE DRATQNISYG AIW 93

(2) INFORMATION ON SEQ ID NO. 197:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 410 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TDQPNIQSVK IHSPLRNPV KGCECPRRD GFGFIKCVDR DVRMFFHFSE ILDGNQLHIA 60  
DEVEFTVVPD MLSAQRNHAI RIKKLPGKTV SFHSHSDHRF LGTVEKEATF SNPKTTSFNK120  
GKEKEAEDGI IAYDDCGVKL TIAFQAKDVE GSTSPQIGDK VEFISIDKQR PGQQVATCVR180  
LLGRNSNSKR LLGYVATLKD NFGFIETANH DKEIFFHYSE FSGDVSLEL GDMVEYSLSK240  
GKGNKVSARK VNKTHSVNGI TEEADPTIYS GKVIRPLRSV DPTQTEYQGM IEIVEEGDMK300  
GEVYPFGIVG MANKGDCLQK GESVKFQLCV LGQNAQTMAY NITPLRRATV ECVKDQFGFI360  
NYEVGDSKKL FFHVKEVQDG IELQAGDEVE FSVIPKSSGG LAGSGACRCF 410

(2) INFORMATION ON SEQ ID NO. 198:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 126 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

LNAILNFFHM EKELLAISYF IVNEAKLIFH TFHCGPAQGC DVVSHSLCIL AQDTQLELDA 60  
LPFLQAIPFV GHPNDAKWID LTFHIALLHN LNHSVLVSLC WINTPQGANY FARVNGGISF120  
LSNAIH 126

00673395-12200

## (2) INFORMATION ON SEQ ID NO. 199:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 85 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

KSHTSCNLLS RPLFVTNTKF NLISYLRRSR SFHILGLKSN SQFHPTVIIS NNAILSLLLF60  
AFIWASGFRI GKSGFFFYRA QKTVI 85

## (2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

ATMRLSVCLL MVSLALCCYQ AHALVCPAVA SEITVFLFLS DAAVNLQVAK LNPPPEALAA60  
KLEVKHCTDQ ISFKKRLLI 79

## (2) INFORMATION ON SEQ ID NO. 201:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00673395-12700



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

SVQCFTSNLA ARASGGGLSL ATWRFTAASL KNKKTVISEA TAGQTRAWAW

50

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 72 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

QVAVEKTLET QVEHFYMSHT HIFSLFPPT FSNEKPFLKR YLIGAVLHFQ LGCKSFWRWI60  
KFGNLEVYRS VT 72

(2) INFORMATION ON SEQ ID NO. 203:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 53 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

SFSPSLTTRA MNSSASSTST CSSYTLGTRL PVGGRGPTKV TCCTSNRLTL SLD

53

002221 55222960

ALVVRFLTKR FIGDYERNAG NLYTRQVQIE GETLALQVQD TPGIQVHENS LSCSEQLNRC 60  
IRWADAVVIV FSITDYKSYE LISQLHQHVQ QLHLGHPAAC GWSWANKSDL LHIKQVDPQL120  
G 121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```

GPLPALAAGS  TFPVLACSSA  MAPKGSSKQQ  SEEDLLLQDF  SRNLSAKSSA  LFFGNAFIVS  60
AIIPIWLYWRI WHMDLIQSAV  LYSVMTLVST  YLVAFAYKNV  KFVLKHKVAQ  KREDAVSKEV 120
TRKLSEADNR  KMSRKEKDER  ILWKKNEVAD  YEATTFSIFY  NNTLFLVVVI  VASFFILKNF 180
NPTVNYILSI  SASSGLIALL  STGSK
  205

```

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 106 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

VLHQDSSPSC LLAPNRPQCL HPLALCLWVA CGIWKSSRVV RVGDTRCFYS LEPLKNPAEC 60  
NSVFVYWLFF DRLLKLNELK GKLRVLGRLL KGKKCLAMCC NKKRRK 106

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

STYGQYVVHC GVEVLQYEEG SNNDHDQEQS VVIEDGKCCS FIISNFILLP QDSFIFLLPR 60  
HLSIISFRKF SSHFFGNSIL PLLCYFVLEN KFHILVCKGY QICAY 105

(i) **SEQUENCE CHARACTERISTIC:**

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

```
(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 208:
LYPNFLVNL ILKQKQRFEE KRFKLDHVS STNGHRWQIF QDWLGTDDQN LDLANVNLML 60
ELLVQKKQL EAESHAALQ ILMEFLKVAR RNKREQLEQI QKELSVLEED IKRVEEMSGL120
YSPVSEDSTV PQFEAPSPSH SSIIDSTEYS QPPGFGSSSQ TKKQPWYNST LASRRKRLTA180
HFEDLEQCYF STRMSRISDD SRTASQLDEF QECLSKFTRY NSVRPLATLS YASDLYNGSS240
IVSSIEFDRD CDYFAIAGVT KKIKVYEDT VIQDAVDIHY PENEMTCNSK ISCISWSSYH300
KNLLASSDYE GTVILWDGFT GQRSKVYQEH EKRCWSVDFN LMDPKLLASG SDDAKVKLWS360
TNLDNSVASI EAKANVCCVK FSPSSRYHLA FGCADHCVHY YDLRNTKQPI MVFKGHRKAV420
SYAKFVSGEE IVSASTDSQL KLWNVGKPYC LRSFKGHINE KNFVGLASNG DYIACGSENN480
SLYLYYKGLS KTLTTFKFDT VKSVLDKDRK EDDTNEFVSA VCVRALPDGE SNVLIAANSQ540
GTIKVLELV
549
```

## 549

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

GTVLSSLTGE YKPLISSTLL ISSSKTLSSF WICSSCSLLF LLATLRNSIR ICSWAACDSA60  
 SSCFFECTSN SNIRLTLAKS RLSWSVPNQS 90

## 90

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

FPSSLLFFFF FFFFCGSIN FYCFVIYFYS KEFVSLSQKL DNTTKSSNVH GVTLMVESWL60  
GIPNVPKVIK EGKEKKKKIF KTNPKPMMTL GRDIT 95

95

## (2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 80 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

KKMVRGLGLF CLLAIYSLW IVCIPYLLSI GLCVDILFLF VQHLLPHLLV TQPLFICGEP60  
IPCGLGEHVT RPYLLSPTAS 80

## (2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 67 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

LKKGKWAKAI HNRKCKWPRN MKRCSSSLIF KEKKEILPTR LAKIFKDSGL ADYRQTGILT60  
NDGVVNW 67

## (2) INFORMATION ON SEQ ID NO. 213:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 78 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

002221"5622960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

SPEVGQALGT AGSRASRKMT SELSSLSISA SIRVSPQTDS LHMAQIQAYM VLGSWDLHKA60  
FFPVVPAEVL LRAFLSLA 78

## (2) INFORMATION ON SEQ ID NO. 214:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 105 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

QAGKRALYKH TQTNTSGDGC VLLEQRLIKH SVCWLSVPLL ENNELGKEQL IRKCALLTVH 60  
ITTKSWQLLK EKGLCRCRSN LSVNSCQQPQ RLPPQHTLIT CVCLA 105

## (2) INFORMATION ON SEQ ID NO. 215:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 216 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes.

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

LSLTSRMEEA ELVKGRLQAI TDKRKIQEEI SQKRLKIEED KLKHQHLKKK ALREKWLLDG 60  
ISSGKEQEEM KKQNQQDQHQ IQVLEQSILR LEKEIQDLEK AELQISTKEE AILKKLKSIE120  
RTTEDIIRSV KVEREERAE SIEDIYANIP DLPKSYIPSR LRKEINEEKE DDEQNRKALY180  
AMEIKVEKDL RTGESTVLSS IPLPSDDFKR SRSKSL 216

00673395-12200

## (2) INFORMATION ON SEQ ID NO. 216:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

FCFFISSCSF PLLIPSRSHF SLKAFFFKCW CFSLSSSIFR RFCEISSCIF LLSVMAWSLP 60  
 FTSSASSILE VKDSQTGKQV QSYHKSRSLG GERSGGDRRE AGRNPLFAPV EK 112

## (2) INFORMATION ON SEQ ID NO. 217:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 339 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

SSQLRRRLVP APAAPRPRPN HGVLGRRLRG DRWQWSHWAK WAMLFASGGF QVKLYDIEQQ 60  
 QIRNALENIR KEMKLEQAG SLKGSLSVVEE QLSLISGCPN IQEAVEGAMH IQECVPEDLE120  
 LKKKIFAQLD SIIDRVILS SSTSCLMPSK LFAGLVHVQKQ CIVAHPVNPP YYIPLVELVP180  
 HPETAPTTVD RTHALMKKIG QCPMRVQKEV AGFVLNRLQY AIISEAWRLV EEGIVSPSDL240  
 DLVMSEGLGM RYAFIGPLET MHLNAEGMLS YCDRYSEGIK HVLQTFGPIP EFSRATAEKV300  
 NQDMCMKVPD DPEHLAARRQ WRDECLMRLA KLKSQVQPQ 339

## (2) INFORMATION ON SEQ ID NO. 218:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

KDPQITQKGI TKIITKIFCP HINMKTTITG CQIILKCNQA EKEKVKISRL SAQVAGNRQP 60  
RERKCCCAAR PRAMIQSDGQ TTGLHHPTQA AHKTASLGSP WAATYVTEG 109

(2) INFORMATION ON SEQ ID NO. 219:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 98 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

LNIPSALRCM VSRGPMNAYR MPNPDMTRS RSLGDTIPSS TSRQASLMIA YCRRFRTPKA60  
TSFWTRMGHC PIFFIRAWVL STVVGAVSGW GTSSTSGM 98

(2) INFORMATION ON SEQ ID NO. 220:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 129 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

TMFFTCGPNE AMVVSGFCRS PPVMVAGGRV FVLPCIQQIQ RISLNTLTN VKSEKVYTRH 60  
GVPISVTGIA QVKLSEFPFH SPLPHHPLSQ TLRHLLATVF STLACREVPL LVSSFPGTFR120  
HLPPPPFFP 129

00422T 56664960



## (2) INFORMATION ON SEQ ID NO. 221:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 118 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

DGDPMAVNL FTLDIEGQCV ERDPLDLLDA GQDKDTPSSH HDWGASAEFG DHHGLIWATS 60  
 EKHGSGWSFR DAGGSPAGVS GRAGSRDLG AGQGPLADQL SWELAPSRVP HPAAPRCC 118

## (2) INFORMATION ON SEQ ID NO. 222:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 119 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

WPSGGPLTSP GQCGSQPPS SPATSDRRPP TSPCSAPGFL PVARVGVGKV WWGSHEVRGK 60  
 AEREGRALSE MLLPFQKKKG GGGKCLGVPG KDTSRGTSI QARVEKTVAR RCLNVWERG 119

## (2) INFORMATION ON SEQ ID NO. 223:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

00673395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

GRRTLFLATF GGYPGSLGCS LSGEANISLV SFFHPLNCKL RITQAHHYSR LGLASQSTLC60  
PACHCCKELL LCQPKQRKYG FSCIIFPFGW FVF 93

## (2) INFORMATION ON SEQ ID NO. 224:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 94 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

NLIYPNSSMY SDTFSEKARI IGAVLSIKGK SSDHLHYNFL CLFSAGEEIH IYSTPHWTLQ60  
NACIFCPSAI CSLPFCLLKE LSNIVFPKMF STGH 94

## (2) INFORMATION ON SEQ ID NO. 225:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 92 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes.

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GHHMHILDRF CTAQLEWVPV TWTGVQYTIC VQYRKPSSAV ARELYSNSLS AQANQVRKTA60  
IWLEDFQETA VPVRGRYYLR GGRGTDIKQE GF 92

## (2) INFORMATION ON SEQ ID NO. 226:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 458 amino acids
- (B) TYPE: Protein

002227 88222960

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

RGKRRRRHRLP ALPPRLLSPS AATMSASAVF ILDVKGKPLI SRNYKGDVAM SKIEHFMPLL 60
VHGEEEGALA PLLSHGQVHF LWIKHSNLYL VATTSKNANA SLVYSFLYKT IEVFCEYFKE120
LEESIRDNF VIVYELLDEL MDFGFPQTTD SKILQEYITQ QSNKLETGKS RVPPTVTNAV180
SWRSEGIKYK KNEVFIDVIE SVNLLVNANG SVLLSEIVGT IKLKVFLSGM PELRLGLNDR240
VLFELTGRSK NKSVELEDVK FHQCVRLSRF DNDRTISFIP PDGDFELMSY RLSTQVKPLI300
WIESVIEKFS HSRVEIMVKA KGQFKKQSVK NGVEISVPVP SDADSPRFKT SVGSAKYVPE360
RNVVIWSIKS FPGGKEYLMR AHFGLPSVEK EEVEGRPPIG VKFEIPYFTV SGIQVRYMKI420
IEKSGYQGPA LGFRYIHPEW AITNFRYQLG RGEEMGGF 458

```

(2) INFORMATION ON SEQ ID NO. 227:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 120 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```

LVTKVGNRPL WVNVAKPQGR ALVTTFLNDL HVSDLDPRDG EVGDLKLDPD GGPALHLFLF 60
HTGEAKVGSH QVLLAPRERL NTPNHVSLR HILGAAHTGL ESGGVGIAGY RHRYLHTVGH120

```

(2) INFORMATION ON SEQ ID NO. 228:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 246 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

09673395-122700

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

GISNLTPMGG RPSTSSFSTL GRPKWARIKY SLPPGKDLIL QITTFLSGTY LALPTLVNL 60  
GESASLGTGT DISTPLATDC FLNCPLALTM ISTRWENFS MTDSIQISGL TWVLRRYDMS120  
SKSPSGGMKE MVRSLKRES RTHWWNFTSS SSTDLFLLRP VSSKSTRSLR PSRSSGIPDR180  
NTLSLMVPTI SLRRTLPLAL TSRLTDSMTS MKTSFFLYLI PSERQDTALV TVGGTRDLPV240  
SSLLLC 246

(2) INFORMATION ON SEQ ID NO. 229:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 275 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

MNTRLQVEHP VTEMITGTDL VEWQLRIAAG EKIPLSQEEI TLQGHAFEAR IYAEDPSNNF 60  
MPVAGPLVHL STPRADPSTR IETGVRQGDE VSVHYDPMIA KWVVAADRQ AALTKLRYSL120  
ROYNIVGLPT NIDFLLNLGS HPEFEAGNVH TDFIPQHHKQ LLLSRKAAAK ESLCQAALGL180  
ILKEKAMTDT FTLQAHDQFS PFSSSSGRRL NISYTRNMTL KDGKNNVAIA VTYNHDGSYS240  
MQIEDKTFQV LGNLYSEGDC TYLKCSVNGV ASKAK 275

(2) INFORMATION ON SEQ ID NO. 230:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 117 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

SEVIILENTI YLFSKEGSIE IDIPVPKYLS SVSSQETQGG PLAPMTGTIE KVFVKAGDKV 60  
KAGDSLMMVI AMKMEHTIKS PKDGTVKKVF YREGAQANRH TPLVEFEFEE SDKRESE 117

00673395 122700

## (2) INFORMATION ON SEQ ID NO. 231:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

SLRFTSNSIN RTFQVSAVSL AVKITKDLES FIFNLHAIRP IMVIRYSYGY IVFTIFKSHV 60  
 SGIRDIQSSS TARRKWRELI MCLKSESVGH GFLEDETQG CLA 103

## (2) INFORMATION ON SEQ ID NO. 232:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 234 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

ADKMFLPLP AAGRVVRRRL AVRRFGSRSL STADMTKGLV LGIYSKEKED DVFQETSAGE 60  
 NFDKLLAGKL RETLNISGPP LKAGKTRTFY GLHQDFPSVV LVGLGKKAAG IDDEENWREG120  
 KENIRAAVAA GCRQIQDLEL SSVEVDPCGD AQAAAEAVL GLYEYDDLKQ KKKMAVSAKL180  
 YGSGDQEAQW KGVLFASGQE LGHANLMGDA SQLRLTPTRF CRNYLRRFSK LVVS 234

## (2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 108 amino acids
  - (B) TYPE: Protein

00/22/95 12:00

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

LPILKIFSNN FGKIWLASIS IGWRLPSNWR AQVLAQKQTG LLSARPPDPH FHRALPTQPS 60  
SFFALGHRIH RDQAPLPPQQ PERLHRDPPP QTRAPGLESA CTPLOQQQL 108

(2) INFORMATION ON SEQ ID NO. 234:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 68 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

CFLCLHASFP VRRFQLPFQR GOLAPRWGSP DADHKRFESS LPSEVVQICS KLSAFQLTI60  
YQNSLLHL 68

(2) INFORMATION ON SEQ ID NO. 235:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 187 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

QRVRAALLSS AMEDSEALGF EHMGLDPRLL QAVTDLGWSR PTLIQEKAIP LALEGKDLLA 60  
RARTGSGKTA AYAIPMLQLL LHRKATGPVV EQAVRGLVLV PTKELARQAQ SMIQQLATYC120  
ARDVRVANVS AAEDSVSQRA VLMEKPDVVV GTPSRILSHL QQDSLKLRDS LELLVVDEAD180  
LLFSLWL 187

007221-5552950

## (2) INFORMATION ON SEQ ID NO. 236:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 76 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

DIGHSDIPST VGSQLLNHGL CLPCQLLGRN KNKASHCLFY HRTCRLPMEQ QLQHRNSISG60  
RLPGARAGPS QEVLPF 76

## (2) INFORMATION ON SEQ ID NO. 237:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 112 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

TGLCNISSLS ACTSSLKVAD MRKALLKSGG KVTRGRLLEL FFKAKGKKEG QLRPPPKAPG 60  
SHEVSGCLAA SGLICEMGSL LPHLASPSAQ LSERLSLQQL RHWPLGHPEH SR 112

## (2) INFORMATION ON SEQ ID NO. 238:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 108 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

004227 00000000

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

CHARLNTDSS RLAMKLLMVL MLAALLLHCY AD SGCKLLED MVEKTINS DI SIPEYKELLQ 60  
EFIDSDAAAE AMGKFKQCFL NQSHRTLKNF GLMMHTVYDS IWCNMKSN 108

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 82 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

LVEETLLEFP HSLCSGITVY ELLKKLFVFR YRYVGIDGLF NHVLQEFAAR ICIAVQEEGR60  
QHEDHQQLHG EAAAVCVQSC VA 82

(2) INFORMATION ON SEQ ID NO. 240:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 48 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

LLFILHQMLS YTVCIISPKE FRVLCDWLRK HCLNFPIASA AASLSMNS

48

(2) INFORMATION ON SEQ ID NO. 241:

00/22T 56E/960



- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 56 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

QAVGEKLSSR DSDLMEDRCF PHFSFSPKKV LLLSPFKQPV SLNFCGHGTD KDPVFS 56

(2) INFORMATION ON SEQ ID NO. 242:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 52 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

IFVAMGQTRT PSSAELRKSP ATSLAIKLQP SHPTRASEEW PLLAGNPLQW AS 52

(2) INFORMATION ON SEQ ID NO. 243:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 67 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

WPKMSQDFSL VQLKTGSLSV PWPQKFRLTG CLKGDRSRTF LGEKEKWGKQ RSSIRSESL60  
 ESFSPTA 67

004221" 46EEZ960

## (2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 64 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

GSSWAEDFKC DISVPKTSLL FAQSCRSMYF LLQYVPIYKF ISHTYNRAHV CTCTRTHTHS60  
LSTR 64

## (2) INFORMATION ON SEQ ID NO. 245:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 74 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

SGPLLPAKNR EVAGLKTLSV TFQFLKHHCY LLKVVGLCIS FSNTSPFISL FPIHTTVHMC60  
ARAHANTHTH SQLV 74

## (2) INFORMATION ON SEQ ID NO. 246:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 69 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

002221-5652950

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

ARIQTPEQHS QVTLFDYNEE MKMGGYLKIG IPSALKVSKL LTCEQHRTPL LWSSEFQLRML60  
QFSKSIYYS 69

(2) INFORMATION ON SEQ ID NO. 247:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 236 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

QLRGGVQRHD RREGEMVCVE LVASDKTNTF QGVIFQGSIR YEALKKVYDN RVSVAARMAQ 60  
KMSFGFYKYS NMEFVRMKGP QGKGHAEMAV SRVSTGDTAP CGTEEDSSPA SPMHERVTSF120  
SRPPTPERNN RPAFFSPSLK RKVPRNRIAE MKKSHSANDS EEFFREDDGG ADLHNATNLR180  
SRSLSGTGRS LVGSWLKLNK ADGNFLLYAH LTYVTLP LHR ILTDILEVRQ KPILMT 236

(2) INFORMATION ON SEQ ID NO. 248:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 161 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

DEEVALGQRQ RGVLPGGRRW SRSAQCNPQA VSVPGHRTV PGRVLAEAEQ SRWKLP SLCT 60  
LNLRHVAAAS DFNHRHPGSSA EAHPPDLAAC GACAEPRPGP ALGVLP SAYL STATGVCDGT120  
PVLEPQPGEA TRLPGP GPTA RTPAQTEVPL TGPAGAASAL C 161

002227-56662960

## (2) INFORMATION ON SEQ ID NO. 249:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 218 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

```

VCIEKEVSIC SVQLQPGPDQ GPSCARQGPR PQVGCIVQIG STVVLP EELL AVVGRVRLH 60
LSDPVP GHLP LEGWGEGRP VVPFWGGGSA EGGHPLVHGR SWAGVLFSP TGGCVTCRHS A120
DRHLGVALAL GALHAHKLHV AVLVEAKRHL LCHAGGHAHP VVIHLLERLV ADGALKDDPL 180
ERVGFVTSHQ LHTDHL SFPT VMSLNTSSKL SIMKKMLG 218

```

## (2) INFORMATION ON SEQ ID NO. 250:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 133 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```

YPQOPPGGAS RRLDDLELC PGEKTAPVWA LSAEEEEAMH FSLAFFLHGS SVFLQITCCH 60
EFLCMRHISS CLYAEVPFIL SIGWWTGERG PRCPTSCASA VGGDRAPRHG GGGHLP HVWG120
GRRHPGTEGS LQR 133

```

## (2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein

00673395-12200

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

RLPSVPGCLR PPQTCGRCPP PPCLGARSPP TALAHDVHGL GPLSPVHQPI ERMKGTSAYR60  
HDEICLMHKN S 71

(2) INFORMATION ON SEQ ID NO. 252:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

RGLQHTDMMK YASCIKHDN MLFAKKQTNH AGKMPGKSAW QLPPQHSQPT QERFSPQDTA60  
PSRPEASVMP LLAGPEGIRA PLLLTVDAAAT HSMQH 95

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 194 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

QKKKMSFRKV NIIILVLAVA LFLVLHNNF LSLSSLLRNE VTDSGIVGPQ PIDFVPNALR 60  
HAVDGRQEEI PVVIAASEDR LGGAIAAINS IQHNTRSNVI FYIVTLNNTA DHLRSWLNSD120  
SLKSIRYKIV NFDPKLLEGK VKEDPDQGES MKPLTFARFY LPILGSQRQR KARLHGVDV180  
ICGRWDFLPF TLQQ 194

00/22T"56E7960

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 109 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

RFHGFPLVRI LLYFSFQKFR VKIDNFVSDA FQGITVEPGP EMVCCIVESN NVENHIGASV 60  
VLNAVYSCNG PPKPVFRCSD DHRNLLLSPY YCMSESIWDK VYRLRPYNS 109

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 57 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

NLAKVKGEMD SPWSSSFTF PSKSLGSKLT ILYLMLFRES LLSQDRRWSA VLLRVTM 57

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 230 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

(2) INFORMATION ON SEQ ID NO. 257:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

(2) INFORMATION ON SEQ ID NO. 258:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 165 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

RVRTLNNCFP VEERSVLFEI LPESAEVEEG SGAGGRDLVL VYGIPVDETQ LGFKILPESV 60  
KVKHPRRRLR VHSIDSTNSV TSSTAPARPL PPIIVSRASK EAIALFAYFP HVAGNSLSSE120  
ALNPRFPAPA GFIPWLFTPG FMSISSAAPT VVAGGGAGAG SLPPL 165

## (2) INFORMATION ON SEQ ID NO. 259:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

ERSHLQPGAV GITESPILGL GSAMTTEIGW WKLTLRKKK STPKVLYEIP DTYAQTEGDA 60  
 EPPRPDAGGP NSDFNTRLEK IVDKSTKGKH VKVSNSGRFK EKKKVRATLA ENPNLFDDHE120  
 EGRSSK 126

## (2) INFORMATION ON SEQ ID NO. 260:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

YVLNTIIVGK GEEKIPHPLP RFGPCSFPLR VCDLPSAKVM AKTGTRNPY HQSSLLQHPN 60  
 RVPGSSVPSA PEGKVPSSL PVLGGELKFS VSASGSTETS PYHVASGKCA LLRIGPGSSH120  
 R 121

## (2) INFORMATION ON SEQ ID NO. 261:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00673395-122700



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

TRVPLYVVVRG RVEDPGISQA LQKWRHINTN LKNSHFLPAG INWPHSFSYG QRGQRGKVLS60  
QIWLMAGSQE V LAPSSALHF DDRPSS 86

(2) INFORMATION ON SEQ ID NO. 262:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 73 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

GSGSPAPRKL HDFALCSAPL CPLFPRETSR SHIFLTDFEA VCLHSDWEHW DHFHHADSGG60  
NGCIPFHDPT CVY 73

(2) INFORMATION ON SEQ ID NO. 263:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 106 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

FVAMCSKQAS LNHGLLGLTL VFLGPLNRHR SGHGKGYIHY HHCRLDENDP SVFNQNNANRQ 60  
LQNQSRKCGI WKSLLERGG R GELSRGRNRA VY AELGTPSL RARGGR 106

00673395-122700

## (2) INFORMATION ON SEQ ID NO. 264:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

VLRWYSSDPS IDTGRVMERD TSITTTVGMM KMIPVFPIRM QTDSFKISQE NVGSGSLSWK60  
EGAEGS 66

## (2) INFORMATION ON SEQ ID NO. 265:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 108 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GCACFRPPSP AGGARTSAGR SPSSADVGSR TQSRSRRRRAA HSRCCVAFPS SFTPRSRRRP 60  
KRRRRRRREND PAASSLPPAH LPCSVSQSAA GARLVLRPRA CGAQAQRP 108

## (2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00673395.122700

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

GAPAFALLLQ REGRGLPRGG VRLVLTAAE PKVDRGGGLH IPVVALRFLP LSLRAHGGGQ 60  
SGGDGGARTT RRPVLFLLRT CPARSVSRP APGLCSDLAL AAPRPSGRS 109

(2) INFORMATION ON SEQ ID NO. 267:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 157 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

IEAAGCTFPL LRCVSFLFHS ALTAAAKAAA TAARERPGGQ FSSSCAPALL GQSVGGRRPA 60  
CAQTSRLRRP GPAAVASVWP ENLGAPAARA PRAEPRSGSR GGRRVSESEG WPGQVVAPRR120  
WSPSKGSVWP TRSTARTSPS AATSPRPREM PPKRRRL 157

(2) INFORMATION ON SEQ ID NO. 268:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 156 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

SSAQGEPEGP GRLLRAPTE SRSEGKSMFA GVPTMRESSP KQYMLGGRV LLVLMFMTLL 60  
HFDASFFSIV QNIVGTALMI LVAIGFKTKL AALTLVVWLF AINVYFNAFW TIPVYKPMHD120  
FLKYDFFQTM SVIGGLLLVV ALPGGVSM D EKKKEW 156

00/22/95 12:27:00

## (2) INFORMATION ON SEQ ID NO. 269:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

LGACSWWWPW ALGVSPWMRR RRSNGSHRSL PAWLRPVAVK DWFGVDSTKL PAFMYPLPFP 60  
 SLGKGTDVLR TLFAETPENR WLSLLWSHSL ASDPSVQASL AAGSLPHAEA LE 112

## (2) INFORMATION ON SEQ ID NO. 270:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 130 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

SQRVCKYSPG SLLPYPRILV RSSNGFRTWV LFSCDHSSAH CMKTGLSQCF NLTRAVSWST 60  
 PRSLLVPYDS PHQMTLAKSR FLCGQGWLAD WWKVGWTKGG HVSSQHQFCT SSASVLVGVP120  
 VSPGPGWARA 130

## (2) INFORMATION ON SEQ ID NO. 271:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 267 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00673395.122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```

GTSGTSHLHP RSICMIQKYN HDGEAGRLEA FSQGESVLKE PKYQEELEDR LHFYVEECDY 60
LQGFQILCDL HDGFSGVGAK AAELLQDEYS GRGIITWGLL PGPYHRGEAQ RNIYRLLNTA120
FGLVHLTAHS SLVCPLSLGG SLGLRPEPPV SFPYLHYDAT LPFHCSAILA TALDVTVPY180
RLCSSPVMV HLADMLSFCG KKVVTAGAI PFPLAPGQSL PDSLMQFGGA TPWTPLCACG240
EPSGTRCFAQ SVVLRGYRQS MPHKPQT                                     267

```

(2) INFORMATION ON SEQ ID NO. 272:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 118 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

QVARVAGPGS HPRTRGRQES CEQSGARDQK LCLIDDRCS GPPHDGRDQV AGPRLLEFPAL 60
NIHLVAALPP SRLPQRSHRA GHTGSGSPAS SHIPPRNAA CPPALPGTWV PLGHFPLG 118

```

(2) INFORMATION ON SEQ ID NO. 273:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 133 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```

LGKATCSRRL PTCTQWGPWG GSSKLHQGIR KGLAWSQGER DDCSCCHHLF PTEAQHVSQM 60
NHGNWRGTQA IRNSDCVQGC SQDGTAVEGQ SGIIMQVREA DRWLGSQAQA PTQGQGADKR120
AVSSQVHETK SCV   133

```

00673395-122700

## (2) INFORMATION ON SEQ ID NO. 274:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 124 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

PQAWRRRLCRC CSARPVAPGA RRLVPCRTPT RQPAGGTCHH PAAFRGRSRH IPVPHALGFG 60  
 ASAGRSVPLQ ALSQSPGAAD LQVFSTGAAP VIHTRLLEDP ILGATLPAGP IRCRAVGLVLP120  
 RHCH 124

## (2) INFORMATION ON SEQ ID NO. 275:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 426 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

GSSRRHGGGY AAVALLVLLL LGPGGWCLAE PPRDSLREEL VITPLPSGDV AATFQFRTRW 60  
 DSELQREGVS HYRLFPAKALG QLISKYSLRE LHLSFTQGFW RTRYWGPPFL QAPSGAELWV120  
 WFQDTVTDVD KSWKELSNVL SGIFCASLNF IDSTNTVTPT ASFKPLGLAN DTDHYFLRYA180

VLPREVVCTE NLTPWKLLLP CSSKAGLSVL LKADRLFHTS YHSQAVHIRP VCRNARCTSI240  
 SWELRQTLSV VFDAFITGQG KKDWSLFRMF SRTLTEPCPL ASESRYVYDI TTYNQDNETL300  
 EVHPPPTTTY QDVILGTRKT YAIYDLLDTA MINNSRNLNI QLKWKRPPEE EAPPVPFLHA360  
 QRYVSGYGLQ KGELSTLLYN THPYRAFPVL LLDTPVPWYLR LLHPLPACPG PAATPPPGDA420  
 DSAAGQ 426

## (2) INFORMATION ON SEQ ID NO. 276:

- (i) SEQUENCE CHARACTERISTIC:

00673395-122700

- (A) LENGTH: 128 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

SPSILYGSCT CHSHKAFGGP DTGGHPSCR P HQVQSCGSGS KTLSLMWINL GRSSVMSSQG 60  
 SSAPLSTSST PPTQSLPLPP SNPWWPMTL TTTFCAMLCC RGRWSAPKTS PPGRSSCPVV120  
 PRQASLCC 128

(2) INFORMATION ON SEQ ID NO. 277:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 481 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

AQDTGGPGRQ SGHGGDLQIP ISLFLRLNT QHWRPGSRKV MAVVPASLSG QDVGSFAYLT 60  
 IKDRIPQILT KVIDTLHRHK SEFFEKHGEE GVEAEKKAIS LLSKLRNELQ TDKPFIPLVE120  
 KFVDTDIWNQ YLEYQQSLN ESDGKSRWFY SPWLLVECYM YRRIHEAIIQ SPPIDYFDVF180  
 KESKEQNFYQ SQESIIALCT HLQQLIRTIE DLDENQLKDE FFKLLQISLW GNKCDLSLSG240  
 GESSSQNTNV LNSLEDLKPF ILLNDMEHLW SLLSNCKKTR EKASATRVYI VLDNSGFELV300  
 TDLILADFL LSELATEVHF YGKTIPWFVS DTTIHDFNWL IEQVKHSNHK WMSKCGADWE360  
 EYIKMGKWVY HNHIFWTLPH EYCAMPQVAP DLYAELQKAH LILFKGDLNY RKLTGDRKWE420  
 FSVPFHQALN GFHPAPLCTI RTLKAEIQVG LQPGQGEQLL ASEPSWWTTG KYGIFQYDGP480  
 L 481

(2) INFORMATION ON SEQ ID NO. 278:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 128 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual

00673395-122700

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

FHISVSTNFS TKGINGLSVC NSFRNLERRE IAFFSASTPS SPCFSKNSLL CRCNVSITLV 60  
KICGILSLIV RYANDPTSCP ERDAGTTAIT FRDPGRQCWV FNRRRNREIG ICKSPPCPDC120  
RPGPPVSC 128

(2) INFORMATION ON SEQ ID NO. 279:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

ELLNQVKGDH RTEIFHIFQW STSWAQRPGA VPLAQAADQP EFQLLMFLWY RVVQDGSHSE60  
PDEMEQKTPI FCHLSTSCNS NHP 83

(2) INFORMATION ON SEQ ID NO. 280:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 168 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00422T" 56552960



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

FYDRRDCFVA VSFLRGLSLW LHFYLWWLCY GGAEMRQKRK GDLSPAELMM LTIGDVIKQL 60  
 IEAHEQGKDI DLNKVKTKTA AKYGLSAQPR LVDIIAAVPP QYRKVLMPKL KAKPIRTASG120  
 IAVVAVMCKP HRCPHISFTG NICVYCPGGP DSDFEYSTQS YTGYEQPP 168

## (2) INFORMATION ON SEQ ID NO. 281:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 70 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

GGTAAMISTR RGWAERPYLE AVLVFTLFRS MSFPCSWASI SCLITSPIVS IISSAGLRSP60  
 FRFCLISAPP 70

## (2) INFORMATION ON SEQ ID NO. 282:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

IDVFPLLVG F NQLFNNISYS QHHQLSRAEI SFPLLPHFCA AVAEPPEIKM QPQTQTTEKA60  
 DSHKTIPPVV K 71

## (2) INFORMATION ON SEQ ID NO. 283:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

00673395-122700

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

KPRQLPNMAF LPSPAWWISL LAVPPQYRKV LMPKLKAKPI RTASGIAVVA VMCKPHRCPH 60  
ISFTGNICVY CPGWDLILIL SIPPSLTGLY EPTSMRSYSV PDMDFFPYRT RTPD 114

(2) INFORMATION ON SEQ ID NO. 284:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 127 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

WVSPLTWASR PCDTEEGRQA MISTRGWAE RPYLA AVLVF TLFRSMSPFC SWASISCLIT 60  
SPIVSIISA GLRSPDYGGF TTRPGSNILG SRVGHYTHQT MEDSPPDQEA TAWAPELATP120  
PCTDEDR 127

(2) INFORMATION ON SEQ ID NO. 285:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 92 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

PHTTNPTCFK LFLIRCPCPV RKRVIWHGI APHGGWLIAQ CKTGWNTQNQ NQVPPRAVYT60  
YISCKTDVWT SVGFAHSHD SNPTSSSDGF RL 92

000221 56667950

## (2) INFORMATION ON SEQ ID NO. 286:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

DLSRPGGTRF VLTIIQQTFFS KVFVQDNFKN NIKINNGFDF SLKIEKKGVG GGVNHWPPFF60  
 WRGPIGIVRP WSGSL 76

## (2) INFORMATION ON SEQ ID NO. 287:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

RTFVLFYHRL TLQLLINTSF GDVWCKTHKH TQKSTSPLHD PSLLSGTISA ASCTLLGPPP60  
 IHRGFRGTQI TAGFQFFFN TFLWSVPTAL SVLLKLE 97

## (2) INFORMATION ON SEQ ID NO. 288:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

002227-5632960

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ILHLEMYGVK HTNTHKKAQA RCMTRL SFLG LFLLRPAPSW AHLRFTEVSG GPKSLLVFNF60  
FLTIHFCGQF QQHCPYF 77

(2) INFORMATION ON SEQ ID NO. 289:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 28 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

ILIDGVRAAF IPYREYNGAR LSRDFISA

28

(2) INFORMATION ON SEQ ID NO. 290:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 28 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

HQFHNYFNLL GFIHLIILKF HQQWGTEK

28

(2) INFORMATION ON SEQ ID NO. 291:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 29 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual

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29

(2) INFORMATION ON SEQ ID NO. 292:

30

(2) INFORMATION ON SEQ ID NO. 293:

33

## (2) INFORMATION ON SEQ ID NO. 294:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 38 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AINKVSSGYG PLALLGFSVS VEAAQRISLN FSQKWLTT

38

## (2) INFORMATION ON SEQ ID NO. 295:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

FTSFNLLIPR TILSTTNRNE ILIHKRKLKT FIAYVGLSNK

40

## (2) INFORMATION ON SEQ ID NO. 296:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

002221"55554950

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

VNLLKYGQIH LAVKQLNIHC YLIKVFVSVL PGPNIKTTSV QKINVQRAVC SLFWYVHFKK60  
 TPLSSLANQE Y 71

## (2) INFORMATION ON SEQ ID NO. 297:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 67 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

REFLYFILSR GTNSRHTFAR PSCRKTQSRK GKNKIAIKYM VLGAGRTRNP QGDQFLARSF60  
 FRVYPVE 67

## (2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 56 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

KNLEFFSPST SYLLQNSSE GFIYILSYPE GPTAGIPLPG LLAERHRAVK AKIKLQ 56

## (2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 140 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

TPNSRGAGRV VRGSARGVGR SCASWLPVGR RCRTSETGSG ASRRSRAIGS PPPSPCPWSA 60  
 NSASSARPTS SSGPKPSFIA FRFGGQSLPP FISLWVQELD FFIWSIYISY ISILRDLKQE120  
 LLMGGQQTIIY SCSSLTGFAS 140

(2) INFORMATION ON SEQ ID NO. 300:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 279 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

QSRSRPRREG VGTGSRAVLC ILATCGSKMS DIGDWFRSIP AITRYWFAAT VAVPLVGKLG 60  
 LISPAYLFLW PEAFLYRFQI WRPITATFYF PVGPGTGFLY LVNLYFLYQY STRLETGAFD120  
 GRPADYLFML LENWICIVIT GLAMDMQLLM IPLIMSVLYV WAQLNRDMIV SFWFGTRFKA180  
 CYLPWVILGF NYIIGGSVIN ELIGNLVGHL YFFLMFRYPM DLGGRNFLST PQFLYRWLPS240  
 RRGVSGFGV PPASMRRAAD QNGGGGRHNW GQGFR LGDQ 279

(2) INFORMATION ON SEQ ID NO. 301:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

002221-566E/960



(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

IDQIKKSSSW THREIKGGSD WPPNLKAIKE GFGPEEEVGR ADEAEFADQG HGDGGGGEPIA 60  
RDRRDAPEPV SDVRHLRPTG SQDAQDRPTP RADPLTTRPA PRLLG 106

(2) INFORMATION ON SEQ ID NO. 302:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 207 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

LEPLEPNRLE LKKGYLTLSD SGDKVAVEWD KDHGVLESHL AEKGRGMELS DLIVFNGKLY 60  
SVDDRTGVVY QIEGSKAVPW VILSDGDGTV EKGFKAEWLA VKDERLYVGG LGKEWTTTTG120  
DVVNENPEWV KVG YKGSVD HENWVSNYNA LRAAAGIQPP GNLIHESACW SDTLQRWFFL180  
PRRASQERYE EGRRAQGRQ PAAERLP 207

(2) INFORMATION ON SEQ ID NO. 303:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 153 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

RWWATRAAWT TRTGCPTTTP CGLLPASSRQ VTSSMSLPAG VTRCSAGSSC RAAPARSATA 60  
RKDDERKGAN LLSASPDEG DIAVSHVGAV VPTHGFSSEK FIPNTDDQII VALKSEEDSG120  
RVASYIMAFT LDGRFLLPET KIGSVKYEGI EFI 153

004227 5666666666

## (2) INFORMATION ON SEQ ID NO. 304:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 174 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

VGTTAPTWLT AMSPKSGEAL SSRLAPLRSS SFLAVALLAG AARQEEPALQ RVTPAGRLMD 60  
 EVTWRLDAGS SPQGVVVGHP VLVVHAALVA HHLHPLRVLV HHITRSGRPL LAQAAHVQTL120  
 VLHCQPFGLA AFLHGAVAVG QNHPPGHGFAA FDLVDDPRPV IHGVEFPIEN NQVG 174

## (2) INFORMATION ON SEQ ID NO. 305:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

KLVCLEADSK SSFSSEHLFS YHLISILKHH GCSCSKMGDV KENYLETFIS SPKWSFILCL60  
 S 61

## (2) INFORMATION ON SEQ ID NO. 306:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 144 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

002221 5552950

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

NTMAVAAVKW VMSKRTILKH LFPVQNGALY CVCHKSTYSP LPDDYNCNVE LALTS DGRTI 60  
VCYHPSVDIP YEHTKPIPRP DPVHNNEETH DQVLKTRLEE KVEHLEEGPM IEQLSKMFFT120  
TKHRWYPHGR YHRCRKNLNP PKDR 144

(2) INFORMATION ON SEQ ID NO. 307:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 128 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

IHQTAFSQMA NEAHFSLIPP GTSASSVFWR IQILTTSVIP SMRIPTVLSS KEHFAKLFYH 60  
RSFLKVFENFF FQSGFQHLIM CFFIIMHRIW PRDFECVFIW NVHRRVVAYY CPAIRSQSKL120  
YVAIIIVW 128

(2) INFORMATION ON SEQ ID NO. 308:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 467 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

SRSKMAALRA LCGFRGVAAQ VLRPGAGVRL PIQPSRGVRQ WQPDVEWAQQ FGGAVMYP SK 60  
ETAHWKPPPW NDVDPPKDTI VKNITLNFEP QHPAAHGVLR LVMELSGEMV RKCDPHIGLL120  
HRGTEKLI EY KTYLQALPYF DRLDYVSM MC NEQAYS LA VE KLLNIRPPPR AQWIRVLFGE180  
ITRLLNHIMA VTTHALDLGA MTPFFWLFEE REKMFEFYER VSGARMHAAY IRPGGVHQDL240  
PLGLMDDIYQ FSKNFSLRLD ELEELLTNNR IWRNRTIDIG VVTAEALNY GFSGVMLRGS300  
GIQWDLRK TQ PYDVYDQVEF DVPVGSRGDC YDRYLCRVEE MRQSLRIIAQ CLNKMPPGEI360  
KVDDAKVSPP KRAEMKTSME SLIHHFKLYT EGYQVPPGAT YTAIEAPKGE FGVYLVSDGS420  
SRPYRCKIKA PGFAHLAGLD KMSKGHMLAD VVAIIGTQDI VFGEVDR 467

00/22T"56E/960

## (2) INFORMATION ON SEQ ID NO. 309:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 131 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

QPSVHEHTHT HTHHTHTTQR PISSEEQAPQ KKLIGRGDQT LLPCSPIYFS KYNILGTYDG 60  
NDICQHVSLR HLVQTSQMGK TRSLDLASIR AAAAIRHQVH PKLSLGLSLNG SICGSWRNLV120  
ALSIQLKVMN Q 131

## (2) INFORMATION ON SEQ ID NO. 310:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 100 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

SQDTMRCWVL GPKVQGNVLH NCVLWRVHII PRWRLPVGCF FAWVHNSSPK LLCPFHIWLP 60  
LPNTSAGLNR QSDSSPRFQH LGRDAPEAAQ SPQRRHLTPA 100

## (2) INFORMATION ON SEQ ID NO. 311:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 162 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

09673395.122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

RRLRGGEPT DRRDPESRT PAPPPTPRAM DPKDRKKIQF SVPAPPSQLD PRQVEMIRRR 60  
RPTPAMLFRL SEHSSPEEEA SPHQASGEG HHLKSKRPNP CAYTPPSLKA VQRIAESHLQ120  
SISNLNENQA SEEDELDEL RELGYPREED EEEEDAARL KS 162

(2) INFORMATION ON SEQ ID NO. 312:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 154 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

VSLGRNLSAL PPLSLAHRHP ACISQEEVEG TSLFPRNPLY PHPVLCSSPR LLGLRLLTSR 60  
RLRLVCVCLF AHLWLIPREP GHLLPDAHPC QSFLHSPSGR WDVROPTLEN PENREQGFAL120  
HNSTPQILSP GHRRPTGQDP KIWGKEVLRT LRYP 154

(2) INFORMATION ON SEQ ID NO. 313:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 101 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AQGLGLFDLR WCPSPALWW GEASSSGEEC SESRNSMAGV GLLRRIISTW RGSSWLGGAG 60  
TENWIFLRSL GSMARGVGGG AGVRDSGSRR RSVLGSPPRR R 101

00222T 566E/960

## (2) INFORMATION ON SEQ ID NO. 314:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 162 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```
SDRWTCSPPL GARSMSRFFA VAGRAPRRQE EGRSRDLQE ERLSAVCIAD REEKGCTSQE 60
GGTTPTFPIQ KQRKKIIQAV RDNSFLIVTG NTGSGKTTQL PKYLYEAGFS QHGMIGVTQP120
RKVAAISVAQ RVAEEMKCTL GSKVGYQVRF DDCSSKETAI KY 162
```

## (2) INFORMATION ON SEQ ID NO. 315:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```
QIGGRARLHS GPGLCPGFPPQ SRAGRQGGRR RVSGQETSRK SGSRLFASPI EKRKDARPRR60
EELLQLFLFR NKEKRLFKL 79
```

## (2) INFORMATION ON SEQ ID NO. 316:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00673395-122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

IGKVGVVPPS WDVHPFSSLS AMQTAESRSS WRSLDRSPSS CRLGALPATA GNRDIDLAPS60  
GGEHVHRSE 69

(2) INFORMATION ON SEQ ID NO. 317:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 173 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

AQESPWQLCR GARTSKRKLP KLGMEQHCNE MCPSSLFLP GAYKAQMYSD VWTNTKKKKK 60  
KKKKKAFLSH RHKTQIIYCY EALFTNGQFL HFIAACERLP DGRPISLVLQ TSSQAAFYQK120  
GENSCLSFLK NAFLYLSIRH YTSELYKRPG GTMSLVDTFH CSVAPFLAWE ASA 173

(2) INFORMATION ON SEQ ID NO. 318:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 96 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

AQESPWQLCR GARTSKRKLP KLGMEQHCNE MCPSSLFLP GAYKAQMYSD VWTNTKKHFL60  
KRKGMSFFLF DKKQVPMKSG AQERWVSHLE AFRTQL 96

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## (2) INFORMATION ON SEQ ID NO. 319:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

TCEPFRNPQV GKDP TPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60  
RDL LLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

## (2) INFORMATION ON SEQ ID NO. 320:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

IRKREQGRSS PAPWESVFAS VPFRGDDGIF DDNFIEERKQ GLEQFINKVA GHPLAQNERC60  
LHMFLQDEII DKSYP TSKIR HA 82

## (2) INFORMATION ON SEQ ID NO. 321:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 159 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

(2) INFORMATION ON SEQ ID NO. 322:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

FTSQPFKVTV SSSNSRFFQL ENRKICLDPD FVSGEAAPAD PHRLRVAHID LEEVAGGSVG 60  
VIQVLR LGDQ PPGVSHGLRH FAVAAAAAAG SLRPLRVOPP PPPLLPVGT RARA 114

(2) INFORMATION ON SEQ ID NO. 323:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 374 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 323:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| RRAQESPLGR | QSHLPRIYQA | FLMSATFNED | VQALKELILH | NPVTLKLQES | QLPGPDQLQQ | 60  |
| FQVVCETEED | KFLLLYALLK | LSLIRGKSL  | FVNTLERSYR | LRLFLEQFSI | PTCVLNGELP | 120 |
| LRSRCHIISQ | FNQGFYDCVI | ATDAEVLGAP | VKGKRRGRGP | KGDKASDPEA | GVARGIDFHH | 180 |
| VSAVLNFDLP | PTPEAYIHRA | GRTARANNPG | IVLTFVLPT  | QFHLGKIEEL | LSGENRGPI  | 240 |
| LPYQFRMEEI | EGFRYRCRDA | MRSVTKQAIR | EARLKEIKEE | LLHSEKLKTY | FEDNPRDLQL | 300 |
| LRHDLPLHPA | VVKPHLGHPV | DYLVPPALRG | LVRPHKKRKK | LSSSCRKAKR | AKSQNPLRSF | 360 |
| KHKGKKFRPT | AKPS       |            |            |            |            | 374 |

## (2) INFORMATION ON SEQ ID NO. 324:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 224 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

QRVRAALLSS AMEDSEALGF EHMGLDPRLL QAVTDLGWSR PTLIQEKAIP LALEGKDLLA 60  
 RARTGSGKTA AYAIPMLQLL LHRKATGPVV EQAVRGLVLV PTKELARQAQ SMIQQLATYC120  
 ARDVRVANVS AAEDSVSQRA VLMEKPDVVV GTPSRILSHL QQDSLKLKRD LELLVVDEAD180  
 LLFSFGFEEE LKSLLEWGRV TCPGFTRLFS CQLLLTRTYK HSRH 224

## (2) INFORMATION ON SEQ ID NO. 325:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 115 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

FFFFFFFFFG AAKIFILLSR GKMPAWKCQG AKGPSTAGPR TVCSGCAVST RASPVHEGCK 60  
 PVLHNVLSSR EAQQPQEGLA VGLNFFPLCL KLRSGFWDFA LLAFLQEEDS FFRFL 115

## (2) INFORMATION ON SEQ ID NO. 326:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

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(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

YLQCQRSLCG AKCVTWAVET RHLLSPALMT LRKEDVIQ GK FLIPKLPVHV NRTSFYSSRC60  
TGSLAP 66

(2) INFORMATION ON SEQ ID NO. 327:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 90 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

FRSCLFMLTG LLFIRQDVLV PWHLKGNPDK GKPVEPFGPI GSQDPSPVFH RYYHVFREGE60  
LEGACRTVSD VRILQSYDQ GNWCVILQKA 90

(2) INFORMATION ON SEQ ID NO. 328:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

SGLLKNHTPV SLIVVALQNS DITHSPAGTF QFSLTEHVV TMKHRTWVLG SYGTKWLNRF60  
AFIRISLKV GNQYILTNNK KSC 83

00/221" 563E/960

## (2) INFORMATION ON SEQ ID NO. 329:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 185 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

ERRSKSREER EKEREREREE RERKRRREEE EREKERARDR ERRKRSRSRS RHSSRTSDRR 60  
 CSRSRDHKRS RSRERRRSRS RDRRRSRSHD RSEKHRRSRS RDRRRSKSRD RKSYPKRSKS120  
 RDREQDRKSK EKEKRGSDDK KSSVKSGSRE KQSEDNTES KESDTKNEVN GTSEDIKSEG180  
 DTQSN 185

## (2) INFORMATION ON SEQ ID NO. 330:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 178 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

YHFPSIQCLC LHS AFLDYRT SHYFFYHQIP SFLSPWIFYL VLCPDFCSCA YMTFDPGFLI 60  
 FFDPDFEICV FFLIDHGFCF FVDLYFCSAF FLYFVTFCGP ETCCIFCLMF GLSVYFVNDF120  
 SFFFLCHEPF LFLFLPLPFV FSFLFLPFLS PVLSLSLCS CFSFLRRSSR IRLFGSSP 178

## (2) INFORMATION ON SEQ ID NO. 331:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 182 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

VSPSDLMSSL VPLTSFLVSL SFDSVFVSSL CFSRLPDFTL LFLSSDPLFS FSLDFLSCSL 60  
 SRLLLLCLYD FRSLFDLLR SRLRDLCLFS DRSWLLLLRR SLLLLRLLSL LRDLLWSRDL120  
 LHLLSDVRLE CLLRERLLFL LSLRALSFS LSSSLRLFL SLSSLSLSRS FSLSSLLLLL180  
 LS 182

(2) INFORMATION ON SEQ ID NO. 332:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 88 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GFGMQLVILR VTIFLPWCFA VPPVPAADHK GWDFVEGYFH QFFLTEKESP LLTQETQTQL60  
 LQQFHRNGTD LLDQMHAHA TAAPLWGA 88

(2) INFORMATION ON SEQ ID NO. 333:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 61 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

PRRSRHSLEP RHKHSSCNNS IGMGQTYLTC RCMLLLQQPH CGVPDGS DNC ISPGRCKWIK60  
 H 61

00673395-122700

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 62 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

STCIFLARCS CRTHQAPHSG AAVAEACICM SSRSVPFRWN CCRSCVCVSW VRSGDSFSVR60  
KN 62

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 61 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

VCPIPMELLQ ELCLCLLGKE WRLLLGQEKI MEIALNKVPS FMVCSRGHWN GETPGQEDSN60  
S 61

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 63 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

AEDTIQKRNS QFETVTPPAP NCGDEERKQW LWFLSEGRRLR TERSNHQGHR FWKSSRGGWL60  
EEQ 63

(2) INFORMATION ON SEQ ID NO. 337:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 65 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

KGWRSDFTVG GRQRDGQHVQ TGSFFSISLL SKSRTAQWLC QGGSSSYSHF SGSLKSTRYY60  
RGSRS 65

(2) INFORMATION ON SEQ ID NO. 338:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 249 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

SCGDVEQKIQ FKRETASLKL LPHQPRIVEM KKGSNGYGFY LRAGSEQKGQ IIKDIDSGSP 60  
AEEAGLKNND LVVAVNGESV ETLDHDSVVE MIRKGGDQTS LLVVDKETDN MYRLAHFSPF120  
LYYQSQELPN GSVKEAPAPT PTSLEVSSPP DTTEEVDHKP KLCRLAKGEN GYGFHLNAIR180  
GLPGSFIKEV QKGGPADLAG LEDEDVIEV NGVNVLDEPY EKVVDRIQSS GKNVTLLVCG240  
KKAYDYFQA 249

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## (2) INFORMATION ON SEQ ID NO. 339:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

ITGVQPEHIQ YLKNYFHLWT RQLAHYHYHYY IHGPKGNEIR TSKEVEPFNN IDIEISMFEK60  
GKVPKIV 67

## (2) INFORMATION ON SEQ ID NO. 340:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 44 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

RIFITTIFMA QKEMKYEYHQ KLNLSLIL KFLCLKKGRY LRLS

44

## (2) INFORMATION ON SEQ ID NO. 341:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 46 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

004227"5657960



(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

KVQLLLMFVF HFLLGHEYSS DKYALTVVSK GGNNFSSTVC VLVVPL

46

(2) INFORMATION ON SEQ ID NO. 342:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 237 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GRWRRRLRHG RGSAAEAVGPT AMAELLQEEL SVLAAIFCRP HEWEVLSRSE TDGTVFRIHT 60  
 KAEGFMDADI PLELVFHLPV NYPSCLPGIS INSEQLTRAQ CVTVKEKLE QAESLLSEPM120  
 VHELVLWQQ NLRHILSQPE TGSGSEKCTF STSTMDDDL WITLLHLDHM RAKTKYVKIV180  
 EKWASDLRLT GRLMFMGKII LDFTTGRQKQ PQGVLDSEN LQSRCGLKWK EMQREND 237

(2) INFORMATION ON SEQ ID NO. 343:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 89 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

YLILLQGDRN NLKVYLILQK TSKVDVDSSG KKCKEKMISV LFETKVQTEH KRFLAFEVKE60  
 YSALDELQKE FETAGLKKLF SEFVLALVK 89

(2) INFORMATION ON SEQ ID NO. 344:

(i) SEQUENCE CHARACTERISTIC:

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- (A) LENGTH: 95 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

PLPKSNAKTT KNTAILLKDS CLPFHFTRAS TNSEKSLSP AVSNSFCNSS NAEYSLTSNA60  
 RNLLCSVCTF VSNSTLIIFS LHFFPLESTS TLEVF 95

(2) INFORMATION ON SEQ ID NO. 345:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 72 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

RAGLFPGRRV GLEAENGPCQ HQHGDFVPCP VLSARMSQPE AEEAALVAHA VGHDCVCSGG60  
 GVLLPHHRRN NL 72

(2) INFORMATION ON SEQ ID NO. 346:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 171 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

GRACFRGGAW GLRPRTALAA TNMETLYRVP FLVLECPNLK LKKPPWLHMP SAMTVYALVV 60  
 VSYFLITGGI IYDVIVEPPS VGSMTDEHGH QRPVAFLAYR VNGQYIMEGL ASSFLFTMGG120  
 LGFIILDRSN APNIPKLNRF LLLFIGFVCV LLSFFMARVF MRMKLPGYLM G 171

## (2) INFORMATION ON SEQ ID NO. 347:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 82 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

EAGCKSFHNI LSIYSVGQES YWPLMPMFIS HRTDTWRFNN NIINYSSGDE EVRHHHQSIH60  
 SHGRRHVQPG RLLQLQVGTF EH 82

## (2) INFORMATION ON SEQ ID NO. 348:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 103 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

HKVIVVWNNI GEKAPDELWN SLGPHPIPVI FKQQTANRMR NRLQVFPELE TNAVLMVDDD 60  
 TLISTPDLVF AFSVWQQFPD QIVGICFLES TSFTFIQGIY SYW 103

## (2) INFORMATION ON SEQ ID NO. 349:

00/22T" 56EE/960

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

ESKNKVWGAD ECVIIYHQC IGQFRKDLE SISHPVCCLL FEDHRDRVGP

50

(2) INFORMATION ON SEQ ID NO. 350:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

SGNCCQTEKA KTRSGVLMSV SSSTINTALV SSSGKTWSRF LILFAVCCLK ITGIGWGP60  
FHNSSGAFSP ILFHTTITL

79

(2) INFORMATION ON SEQ ID NO. 351:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 70 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

004227 5652960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

GTLRHSVHV V PPKHGHKKVL SSGVCSRLLG IQREGRNQEF QKHIHVATPA TSGILCSDKL60  
HGWEVFFLAR 70

## (2) INFORMATION ON SEQ ID NO. 352:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

HLIPFMAKSS FRVGNTQTFC ACCSPKAWSS QSPEFWCVLP PPGYTERRQE SGVPEAYTCG60  
YPSNKRHPVL R 71

## (2) INFORMATION ON SEQ ID NO. 353:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 60 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes.

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

SGQCGMQLGP DQPSSEQMAV VPISTKPQRA RKNTSQPCSL SEHRMPLVAG VATCICFWNS60

## (2) INFORMATION ON SEQ ID NO. 354:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 225 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

002221-5552950

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

```
GLPARRPQCF LRAEMANSGL QLLGFSMALL GWVGLVACTA IPQWQMSSYA GDNIITAQAM 60
YKGLWMDCVT QSTGMMSCMK YDSVLALSAA LQATRALMVV SLVLGFLAMF VATMGMKCTR120
CGGDDKVKKA RIAMGGGIIF IVAGLAALVA CSWYGHQIVT DFYNPLIPTN IKYEFGPAIF180
IGWAGSALVI LGGALLSCSC PGNESKAGYR APRSYPKSNS SKEYV 225
```

(2) INFORMATION ON SEQ ID NO. 355:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 111 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```
QHHHGPGHVQ GAVDGLRHA E HGDDELQNVR LGARPVRGLA GHSSPNGGLP GAGLPGHVCG 60
HDGHEVHALW GRRQSEEGPY SHGWRHNFHR GRSCRLGSL L LVWPSDCHRL L 111
```

(2) INFORMATION ON SEQ ID NO. 356:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 154 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

```
CCHPHRSSSA TAGWRCRPPD PPSPAGPWRS PATAGPNWPF PPSENTGGAG RGDPTVKQTT 60
LGGQPHKRKL EVEFSGHPKR QKGFGPGECK SCHQTTHKST PPVKRWPRGT GSRIRREGGS120
RQNWWSPKAR RFPPGALGDP LSPPASRLLT GVGP 154
```

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## (2) INFORMATION ON SEQ ID NO. 357:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 72 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

NLTQVTFLFF CPPNVHASR LHFEALMNIP VLVLDVNDDF AEEVTKQEDL MREVGRTLTP60  
VFLVSLWLY LL 72

## (2) INFORMATION ON SEQ ID NO. 358:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 69 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

SPSHLSHEVF LFGYFLSKII IDIQHQHWNV HQSLKVEPIR SVNVWGTEKK KCNLSQVSHT60  
RQVLLREQI 69

## (2) INFORMATION ON SEQ ID NO. 360:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 53 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

00/22T"56E2960

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

KRYNQRETR KTGKVLPTS LMRSSCLVTS SAKSSLTSNT STGMFIRASK WSL

53

(2) INFORMATION ON SEQ ID NO. 361:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 111 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

SCWETKWTSC PRMLLATGRG CGSDCGRTVP APGSCWPLAP RATAPRQGRA TGRGESESAE 60  
LVPHSGQGRA ADQRQDLWS GRVDLCPSAL LALPWGRLLS GRHQRRQIHS L 111

(2) INFORMATION ON SEQ ID NO. 362:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 109 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

TRNGSVFGCY RPHRFAGKS VSLVYSRGFQ HPPCAYHLLG QGRRSVSEAC RSYVTPDSNG 60  
WKRTNGQDFL LLLKTLMKV RKGWGPSS GPTSKFPLQV ILCQALFKK 109

(2) INFORMATION ON SEQ ID NO. 363:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 381 amino acids

00222T"56E7960



(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GPARRPAARL ARAGGPQAAD RAGKQSGPPA PGCSWLPAEA AGATVGGLCP RRAPAGPWHQ 60  
 GPQRPVKDEP QDGENPNPPN WSRTVVRDVR LISAKTGYGV EELISALQRS WRYRGDVYLV120  
 GATNAGKSTL FNTLLESYDC TAKGSEAIDR ATISPWPGTT LNLLKFPICN PTPYRMFKRH180  
 QRLKKDSTQA EEDLSEQEQN QLNVLKKHGY VVGRVGRFTL YSEEQKDNIP FEFDADSLAF240  
 DMENDPVMGT HKSTKQVELT AQDVKDAHWF YDTPGITKEN CILNLLTEKE VNIVLPTQSI300  
 VPRTFVLKPG MVLFLGAIGR IDFLQGNQSA WFTVVASNIL PVHITSLDRA DALYQKHAGH360  
 TLLQIPMGKK ERMGRISSC C 381

(2) INFORMATION ON SEQ ID NO. 364:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 182 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

QPSTTCTSVL VCLLSAMPLP VALQTRLAKR GILKHLEPEP EEEIIAEDYD DDPVDYEATR 60  
 LEGLPPSWYK VFDPSGLPY YWNADTDLVS WLSPHDPNSV VTKSAKKLRS SNADAEKLD120  
 RSHDKSDRGH DKSDRSHEKL DRGHDKSDRG HDKSDRDRER GYDKSRNGIR DRGYDQADRE180

EG

182

(2) INFORMATION ON SEQ ID NO. 365:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 149 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

09673395.122700

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

RRHERDGRCD SLPLPARVYW SVCYQLCRCP LACRPAPWPRE ASSNIWSLNQ RKRSLPRTMT 60  
MILWTTRPPG WRAYHQAGTR CSTLPAGSLT TGMQTQTLYP GSPHMTPTPW LPNRPRSSEA120  
VMQMLKKS WT GAMTSRTGAM TSRTAAMRN 149

(2) INFORMATION ON SEQ ID NO. 366:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 80 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

PRSRSLSDLS WPRSDLSWPL SSFSWLRSDL SWPLSDLSWL RSNFSSASAL LLLSFLADLV60  
TTELGSCGES QDTRSVSAFQ 80

(2) INFORMATION ON SEQ ID NO. 367:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 160 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

VAQQPALIHG YRKAULTPNH VEFSLRYDAV LRGPMDSDDS HGSVLRLSQA LGNVTVVQKG 60  
ERDILSNGQQ VLVCSQEGSS RRCGGQGDLL SGSLGVLVHW ALLAGPQKTN GSSPLLVAAF120  
GACSLTRQCN HQAFQKHGRS TTTSDMIAEV GAAFSKLFET 160

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## (2) INFORMATION ON SEQ ID NO. 368:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 164 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ILNGNQFMLK LKIWQAPYAF STRVGPDPFPI THTLSPVQGA CLLVCAGSG FKELAEAGGPH 60  
LGDHVGGGGG ATVLLEGLVV ALPGERAGAK RGHQERAGPI CFLWSSKERP VYQDAQGARQ120  
EVPLPSTPAA AAFLAAHKHL LAVGEDVALS FLDHRHVAQG LAES 164

## (2) INFORMATION ON SEQ ID NO. 369:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 187 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

KSGKHRTPSA HAWVRIFPSH TRSPPSKVPV YFWSARAQVS KSLKKAAPTS AIMSEVVVER 60  
PCFWKAWWLH CLVREQAPNA ATRRGLDPFV FCGPARSAQC TRTPREPDRR SPCPPHLRLL120  
PSWLHTSTCW PLERMSRSPF WTTVTLPRAW LSLSTDPWLS SLSIGPLSTA SYSLLNSTWL180  
GVSTAFR 187

## (2) INFORMATION ON SEQ ID NO. 370:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 40 amino acids  
    (B) TYPE: Protein

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(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

LFLFTNHNDS GKPGCKHQHC HQLRICDQEC HLTVTGRRQK

40

(2) INFORMATION ON SEQ ID NO. 371:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 34 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

QAEDKSETGL MRITGKLALA PPENELFHSL ADHP

34

(2) INFORMATION ON SEQ ID NO. 372:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 38 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

NSSFSGGAKA SFPVIRISPV SLLSSACYRE MALLITDP

38

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## (2) INFORMATION ON SEQ ID NO. 373:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 123 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

RQLFGIVSIA TLTVLAYERY IRVVHARVIN FSWAWRAITY IWLYSLAWAG APLLGWNRYI 60  
 LDVHGLGCTV DWKSKDANDS SFVLFLFLGC LVPPLGVIAH CYGHILYFHS NASLVWKIFRI20  
 QFK 123

## (2) INFORMATION ON SEQ ID NO. 374:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 121 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

TVHSRGPCQS DQFFLGLEGH YLHLALLTGV GRSTSPGMEQ VHPGRTRTRL HCGLEIQGCQ 60  
 RFLCAFLIS WLPGGAPGCH SPLLPYSIF PFECFVGVED LQTIQVIKIL KYEKKLAKMC120  
 F 121

## (2) INFORMATION ON SEQ ID NO. 375:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 58 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

004221"5652960

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

HPGAPPGSQE IRKAQRRNRW HPWISSPQCS LVRVRPGCTC SIPGEVLLPT PVSRARCR 58

(2) INFORMATION ON SEQ ID NO. 376:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 49 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

AFTCDFVPLC GLLEQWTTKS AMQFIKVDLV ICHPTAYGPC KPVLEANIL

49

(2) INFORMATION ON SEQ ID NO. 377:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 68 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

FCTTLWPSGA MDNQVSYAVH KSGPGYMSSN SIWSLQACFG SQYSITYRNP LESDVFGSNI60  
FSQGSNGL

68

(2) INFORMATION ON SEQ ID NO. 378:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 64 amino acids

004221"56557960

(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

HITRSTEMNC IADLVVHCSR RPQSGTKSQV KAQTAPVILV VLSLHSSPLA KTGLNMKSPA60  
 PRPQ 64

(2) INFORMATION ON SEQ ID NO. 379:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 144 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

APISSNFCSE SIWGYCDQLK VSESTHVLQP FLPSILDGLI HLAAQFSSEV LNLVMTLCI 60  
 VCTVDPEFTA SMESKICPFT IAIFLKYSND PVVASLAQDI FKELSQIEAC QGPMQMLIP120  
 TLVSIMQAPA DKIPAGLCAT PLIS 144

(2) INFORMATION ON SEQ ID NO. 380:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 254 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

09673395-122700

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

YEIQSLPFPS FSSAKLSLLW HSPVFTQMTM PSVQNGGECL RAYVSVTLEQ VAQWHDEQGH 60  
 NGLWYVMQVV SQLLDPTSE FTAAFVGRV STLSKAGRE LGENLDQILR AILSKMQQAE120  
 TLSVMQSLIM VFAHLVHTQL EPLLEFLCSL PGPTGKPALE FVMAEWTSRQ HLFYGGYEGK180  
 VSSVALCKLL QHGINADDKR LQDIRVKGEE IYSMDEGIRT RSKSAKNPER WTNIPLLVKI240  
 LKLIINELSN VMGG 254

(2) INFORMATION ON SEQ ID NO. 381:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 95 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

SLSGPNANEA DSHSGQHNAG PSRQDSCRAL CDTIDILTTV VRNTKPPLSQ LLICQAFPAV60  
 AQCTLHTDDN AISAEWRRVL AGLCVSDPGT SSPVA 95

(2) INFORMATION ON SEQ ID NO. 382:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 263 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

APISSNFCSE SIWGYCDQLK VSESTHVLQP FLPSILDGLI HLAAQFSSEV LNLVMETLCI 60  
 VCTVDPEFTA SMESKICPFT IAIFLKYSND PVVASLAQDI FKELSQIEAC QGPMQMRLIP120  
 TLVSIMQAPA DKIPAGLCAT PIDILTTVVR NTKPPLSPLL ICQAFPAVAQ CTLHTDDNAT180  
 MQNGGECLRA YVSVTLEQVA QWHDEQGHNG LWYVMQVVSQ LLDPTSEFT AAFVGRLCFH240  
 PHLQGRAGTR GESRPDFFVP SFS 263

00722T"5662960



## (2) INFORMATION ON SEQ ID NO. 383:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 68 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TLRCGGPGAG SPLASHTTVH CGPAHHATGL LVPGLSLTHRP ASTLRHSAWW HCHLCEGYTV60  
PQQGKLGR 68

## (2) INFORMATION ON SEQ ID NO. 384:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 97 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

HIGPQALSAI LHGGIVICVK GTLCHSRESL ADEKLGKGRL CISYYCCQDI NGCRTKPCRN60  
LVCWGLHYAD QSGNQPHLHW ALTGFNLGQL LEDVLSQ 97

## (2) INFORMATION ON SEQ ID NO. 385:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 140 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

TRSSSPQTIT FDACVVIPCG DLQSQKQLSD SEKYLCPFKI KGSPYQDPCS LTNAGKQVCH 60  
SWNEVVWTE YQGWTSSSTGG CMSLKPYIHF TKESTPHNCQ YNQCNPVQIS ILIPTSTDPK120  
PTLSCGIWHG SRNSRGTSYW 140

(2) INFORMATION ON SEQ ID NO. 386:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 49 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

DVPLLFR LPC HIPQLKVGLG SVEVGMRIEI CTGLHWLYWQ LWGVLSLVK 49

(2) INFORMATION ON SEQ ID NO. 387:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 51 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

SECMVLR TYN HRLTRSSLDI QLSTPPHSSY GRPVFLHSLR NKGLDRGSLL S 51

(2) INFORMATION ON SEQ ID NO. 388:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 97 amino acids

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(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

SSSPLSFCWF LPSPAASCSS SCPSGMTSWS RSGPSISGFS WLTDRAACTC GVWPSSPAPP60  
 KPLPPTGLSS TPAPGLAPAA ACPSEAPINT DLMVPFP 97

(2) INFORMATION ON SEQ ID NO. 389:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 148 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GKGTMRSVLI GASEGQAAAG ARPGAGVEDR PVGGRGFPGA GELGQTPQVQ AALSVSQENP 60  
 EMEGPERDQL VIPDGQEEEQ EAAGEGRNQK KLRGEDDYNM DENEAESETD KQAALAGNDR120  
 NIDVFNVEDQ KRDTINLLDQ REKRNHTL 148

(2) INFORMATION ON SEQ ID NO. 390:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 84 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

00673395-122700

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GPRDRLIQPS YFQRGKWGLE VTEHLAGALA PLASHRLPSS WDYRHTVTEA GPVCNSRCHL60  
QLKHSSYVMS LVTKVKLSHP EKAT 84

(2) INFORMATION ON SEQ ID NO. 391:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 59 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

CGKKCITLFL FLSPSLPLWC LRYWGSHSWG HSEATRNASS LHLAVSARTR NPQTSSQTS 59

(2) INFORMATION ON SEQ ID NO. 392:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 107 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TPRNLNFHRSK LTQFHCVNTV SLGSTKHPIT QFCFIVWTPS RLQGHGQEV CEEVCGFLVL 60  
ALTARCKLEA FLVASEWPQL WDPQYLRHHR GREGDRNRNR VMHFFPH 107

(2) INFORMATION ON SEQ ID NO. 393:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 61 amino acids
- (B) TYPE: Protein

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(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

VAPAVGSPVS QAPQRQRGGQ EQKQSYAFLS TLKKRNYTFR GMLSPRSTSS PVFHDLPKK60  
I 61

(2) INFORMATION ON SEQ ID NO. 394:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 74 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

CNCAPSLPDF SPLHPQCGIS LVPRGTPLDL WTSRPGQEAA TRNPRPLLLK FTASVVVPDS60  
SPAPGTTSTW GGAF 74

(2) INFORMATION ON SEQ ID NO. 395:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 112 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

ATVHPACQIF PHYTPSVAYP WSPEAHPLIC GPPGLDKRLL PETPGPCYSN SQPVWLCLTP 60  
RQPLEPHPPG EGPSEWSSDT AEGRPCPYPH CQVLSAQPGS EEELEELCEQ AV 112

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## (2) INFORMATION ON SEQ ID NO. 396:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 45 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

DRRSHGLLLY NLPGEQFKNM NQDPFDPLII QKSTQKYAQK YVGIH

45

## (2) INFORMATION ON SEQ ID NO. 397:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 43 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

ERLSHCRLSV MLALISLCTP CTHAFSPVFY QASVSCITLK CDH

43

## (2) INFORMATION ON SEQ ID NO. 398:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 64 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

WIKRILIHIF KLLSREVVKQ QSMRASISLP LLGDACPHLP MYPMHSCLLS CFLSSLSFMY60  
YTKM 64

## (2) INFORMATION ON SEQ ID NO. 399:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

HIKIEFFGQN FWEAMHPTWA DIQPELFSRG EWYWQFMAEI HSDWLESMLY QLLNILSITL60  
AYCYYYISSI YRQKGHF 77

## (2) INFORMATION ON SEQ ID NO. 340:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

SSLGKTFGKQ CILHGLIFSL SCSQEESEGTG SLWLKSILIG WSLCYTSC

48

## (2) INFORMATION ON SEQ ID NO. 401:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

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(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

FRNPALIEPS VGSTAEIFRA FNILKMAFLS IYRGNIIVTV CKSDTQNV

48

(2) INFORMATION ON SEQ ID NO. 402:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 70 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

EQLRLNISPC RMHCFPKVLP KELYFYVLSH RTGEKCSGHC WDLIFLGMGS GLMILATGVQ60  
ENGSPGSDSW 70

(2) INFORMATION ON SEQ ID NO. 403:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 63 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

MCDFIRGICQ FSHCGSFSD F ACSSSKEARS FADFTIPQTC KFLTSSKLAL ALSSTFPFKS60  
NLC 63

(2) INFORMATION ON SEQ ID NO. 404:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 71 amino acids

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(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

MGITHECVIL LGASANSLTV VPSLTLPVHH LRRLDPSLTS PFLKPVSESL LPNWLWLFLQ60  
PFHSRAIFAK E 71

(2) INFORMATION ON SEQ ID NO. 405:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 63 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

LGDDHIYNWDV NHFFSGIRAQ RHNLQGHIIY YEHFTVRLFI LPSTCAEMKP KQAVGFHKSI60  
YVG 63

(2) INFORMATION ON SEQ ID NO. 406:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 88 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

LVEPNGLFWF HFSASRRQNK ESHSKMFIVD NMSLKVVPLC SYSTEEMIHI PIIDMVSQSE60  
 ESFRRLHKYV LCTCPMLGNR KIIVIDKT 88

## (2) INFORMATION ON SEQ ID NO. 407:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 269 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

LTVVYTVFYA LLFVFIYVQL WLVLRYRHKR LSYQSVLEFL CLEWASRRTV LFSFYFKDFV 60  
 AANSLSPFVF WLLYCFPVCL QFFTLTLMNL YFTQVIFKAK SKYSPELLKY RLPLYLASLF120  
 ISLVFLLVNL TCAVLVKTGN WERKVIVSVR VAINDTLFVL CAVSLSICLY KISKMSLANI180  
 YLESKGSSVC QVTAIGVTVI LLYTSRACYN LFILSFSQNK SVHSFDYDWY NVSDQADLKN240  
 QLG DAGYVLF GVVLFVWELL PTTLVVYFFR VRNPTKDLTN PGMVPSHGFS PQILFL 296

## (2) INFORMATION ON SEQ ID NO. 408:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 152 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

HRRLHRVLRA ALRVHLRAAL AGAALPPQAA QLPERLPLSL PLLGLPADRP LLLLLQRLRG 60  
 GQFAQPLRLL AALLPCVPA VFHPHADELV LHAGDFQSQV KIFSRTIQIP VAPLPGLPLH120  
 QPCFPVGEFN LCCAGKDGKL GEEGYRLCAS GH 152

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## (2) INFORMATION ON SEQ ID NO. 409:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

LGFENHLREV QVHQREGEKL QAHREAVEQP EDEGAERIGR HEVFEVEGEE DGPPGGPEEA 60  
EKEEDALVAE PLVAVTQHQP ELHVDEHEEQ RVEHGVDDGE 100

## (2) INFORMATION ON SEQ ID NO. 410:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 268 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

APISSNFCSE SIWGYCDQLK VSESTHVLQP FLPSILDGLI HLAAQFSSEV LNLVMETLCI 60  
VCTVDPEFTA SMESKICPFT IAIFLKYSND PVVASLAQDI FKELSQIEAC QGPMQMLRIP120  
TLVSIMQAPA DKIPAGLCAT AIDILTTVVR NTKPPLSQLL ICQAFFPAVAQ CTLHTDDNAT180  
MQNGGECLRA YVSVTLEQVA QWHDEQGHNG LWYVMQVVSQ LLDPRTSEFT AAFVGAFVST240  
LISKAGRELG ENLDQISSCH PSVKMAGG 268

## (2) INFORMATION ON SEQ ID NO. 411:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein

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(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

HIGPQALSAI LHGGIVICVK GTLCHSRESL ADEKLGKGRL CISYYCCQDI NGCRTKPCRN60  
LVCWGLHYAD QSGNQPHLHW ALTGFNLGQL LEDVLSQ 97

(2) INFORMATION ON SEQ ID NO. 412:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 77 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

PPAILTEGWH EEIWSRFSPS SRPALEMRVE TKAPTKAAVN SEVRGSRSWL TTCITYHSPL60  
WPCSSCHWAT CSRVTDT 77

(2) INFORMATION ON SEQ ID NO. 413:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 62 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

IGFASIPPRI SGSPSILLAF YPHPPSPKLG PVLLCARETP KFRKRSIFYR GGFILDQKNK60  
KN 62

002221"5652960

## (2) INFORMATION ON SEQ ID NO. 414:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 65 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

DLIYNYCYCP SDLSFSAIDV IAISRSSHNV FNPALILMLR MEFLTSSLKE PQPPNTYTYT60  
SRIAK 65

## (2) INFORMATION ON SEQ ID NO. 415:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

LDLSPFHVVF PDPHPSEFWLF TRIRHLRSWG QCYVVPKGPR NLGENQYFTG EDSSLTKKIK60  
KIKNTKKFMF LYCIPKECLY TVIILKENTS MLDI 94

## (2) INFORMATION ON SEQ ID NO. 416:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GRRNDQLNLH IPQAGPFAGP YRLGWPLLSS GIRLPDWLVL HVSIKLKVIP WPPFGENQPH60

PASWGQWGRD FGLSEQLLEA AHD

83

(2) INFORMATION ON SEQ ID NO. 417:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 93 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

RRKASIIAFK GILLTLTQGV QSAREPILIS SSKMELEENP WNVLKDVSGV RSSMWLAKGH60  
LYLFQLEFIN SCSLVSLGAE VWHIFKPVHS RIQ 93

(2) INFORMATION ON SEQ ID NO. 418:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 96 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

TLNPHKTLA KKAARVIFFCI QDSTANLVFC YKNLVSHFLL KRTRITGTHP QLHETPSFLN60  
EHESIYVHPS THMKMLCSST GMDGIRIKPI WKLKYF 96

00673395 122700

## (2) INFORMATION ON SEQ ID NO. 419:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

YSFFFFLYQN NHLPLFFLER EEESGEEGKN AKCHFELLVH HTRGSPLMSA ASVHRPQVKE60  
RMRSSWTS 68

## (2) INFORMATION ON SEQ ID NO. 420:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

KPSIHFFFSK TKTIIFLYFS WSGKRRVEKK GRMQSVTLNF SFTTHVGVHS CQQPPCTGPR60

## (2) INFORMATION ON SEQ ID NO. 421:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN

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(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

DAGCRFVAPA LSGSPEITPQ RQLPFVNTRQ AVLAGPTRPH SFFHLGPVHG GC

52

(2) INFORMATION ON SEQ ID NO. 422:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 52 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

VLGKSSMSIT IVWKANLHPK QIEVSQVKPH RMANRCLGCR MQVRGPGPVW LP

52

(2) INFORMATION ON SEQ ID NO. 423:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 59 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

YRYVFPTTHY GYNGVELQTV KFCFGLVSPD PPRQELPLPP YLPALKLCPI KLDTNLTGF 59

(2) INFORMATION ON SEQ ID NO. 424:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 79 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

004221-5652950



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

VTCLSLYVET NFTMITDLN ISSLNFTIL KLLGKLPF CSKGALHLLK PWGHTSSVAS60  
EGQILWVVG DNFVLTYVIL 79

(2) INFORMATION ON SEQ ID NO. 425:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 102 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

HKKTSSYSGV TVCSYDSIIR LKAGEICVQF NRTQLKGRQV GWERKLLSGG IRGNQSKTKF 60  
-YCLQFNSIIA IMCSGKHIPV LLDRVSFPFS GTKMVEGIIN PT 102

(2) INFORMATION ON SEQ ID NO. 426:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 81 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

SMPFQFGTQP RRFVVEGGDS SIELEPGLSS SAACNGKEMS PTRQLRRCPG SHCLTITDVP60  
VTVYATTRKP PAQSSKEMHP K 81

00673395-122700

## (2) INFORMATION ON SEQ ID NO. 427:

(i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 62 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

GRASALACHR YRSDWASGLY ILAALSTSSS IGSSGGRGNW QQVGNYVKES PDVIISGCHR60  
NI 62

## (2) INFORMATION ON SEQ ID NO. 428:

(i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 100 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

REHQLLSGND FQGTSGVAWL VTSPSHYRQH WSSAQVPAQL KNLLPLETS LAGFQIEKAY 60  
FTENQKRLSL IPVEVNKSM L STGLSTEGWN CQRNDDQMFR 100

## (2) INFORMATION ON SEQ ID NO. 429:

(i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 40 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

NSHLNVTLLII IMLIFSISYR NQSLCLKLHRG LKNVYHSIFI

40

(2) INFORMATION ON SEQ ID NO. 430:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 31 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GGIGYKGRYL NSSNNGYNPF FHNHLGCFKA I

31

(2) INFORMATION ON SEQ ID NO. 431:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 53 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

TLPIIRDAKN QHNYQCHIQ VGILPNTTIK GRIKLDNLIK KYKAFKNLTH HLK

53

(2) INFORMATION ON SEQ ID NO. 432:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 31 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

IALKHPKWLW KKGLYPLFEL FRYLPLYPIP P

31

(2) INFORMATION ON SEQ ID NO. 433:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 85 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

CNIFQWGPSE HTCWTVQTIS SPEGKYFCIR GNSVLERNMF FISQIKTLSN GKLASNFFKY60  
SIFFSPLVVT GFYRSSYTVC FNSGP

85

(2) INFORMATION ON SEQ ID NO. 434:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 81 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

LLIREINQVF PLIYDAIYFS GGLQSTPVGR CKPYLLQKAN TfvSEETQFW RGICSLYLKS60

KLSLMVNWLL IFLSTVFFFP L

81

00673395-122700

## (2) INFORMATION ON SEQ ID NO. 435:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 95 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

YKSICLLEKI WFAPSNRCAL KAPTEIYCII DEGKDLVNFS YQKLVFRTSC PTWLPGAQGF60  
FSEIVLRDPQ TCSPSPGATC ASSPRRQAVR SMRLS 95

## (2) INFORMATION ON SEQ ID NO. 436:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 81 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

SCAFLLLWGH SGPTWASMDP GLEQAHLHLF HLRQCGSRCQ EGLTSGPSRF LCARNERP60  
ILPPRLDPEV RAGQPSRKHT V 81

## (2) INFORMATION ON SEQ ID NO. 437:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 94 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

09673395-122700

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

SRWNDSHPLL ISPLTSLKLL SSSKSHCQLP YVVLGPPEPW NLAPWGGLIP AREHSCFSRD60  
TVACMGQHGP WADHVHSCFS GDTVGPHGPA WTLG 94

(2) INFORMATION ON SEQ ID NO. 438:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 91 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

HLEPHCLRWK RWRACSSPG SMLAHVGPLC PQRSRNAHDQ PRVHAGPCRP LCPLRSRNAL60  
VPELNHPRVP GSKAPWDPEP HTEVGNGSLM S 91

(2) INFORMATION ON SEQ ID NO. 439:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 456 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

ITKTHKVDLG LPEKKKKKKV VKEPETRYSV LNNDYFADV SPLRATSPSK SVAHQAPEM 60

PLVKKKKKKK KGVSTLCEEH VEPETTLPAR RTEKSPSLRK QVFGHLEFLS GEKKNKKSPL120  
AMSHASGVT SPDPQGEER TRVGKKLKKH KKEKKGAQDP TAFSVQDPWF CEAREARDVG180  
DTCVSGKKDE EQAALGQKRK RKSPREHNGK VKKKKKIHQE GDALPGHSPK SRSMESSPRK240  
GSKKKPVKVE APEYIPISDD PKASAKKKMK SKKKVEQPVI EEPALKRKKK KERESGVAGD300  
PWKEETDIDL EVVLEKKGNM DEAHIDQVRR KALQEEIDRE SGKTEASETR KWTGTQFGQW360  
DTAGFENEDQ KLKFLRLMGG FKNLSPSFSR PASTIARPNM ALGKKAADSL QQNLQRDYDR420  
AMSWKYSRGA GLGFSTAPNK IFYIDRNASK SVKLED 456

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## (2) INFORMATION ON SEQ ID NO. 440:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

```
VRVCFLLP RV SCYPTLSLLL FLPFQSWLLD DWLLYLLFGL HLFLCGGLRV ITYGDVFRSL 60
NFDWLLFTSF PRAALHGPGG LGVAWEGISL LVDEFFLLHL PIVESGALPL PFLPQGCLFL120
ILLPH 125
```

## (2) INFORMATION ON SEQ ID NO. 441:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 381 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

```
SRCRFCCRLS AAFLLPRMLG LAIVLAGRLN EGDRFLKPPI SLRNFSFWSS FSKPAVSHWP 60
NWVPVHFLVS EASVLPDSRS ISSCKAFRLT WSMCASSMLP FFSNTTSKSV SVSSFQGS PA120
TPLSLSEFFF LFRAGSSMTG CSTFFLDFIF FFAEALGSSL MGMYSGASTL TGFFLLPFLG180
LLSMDLEGLE WPGRASPSWW IFFFFFTFPL CSLGLFRFRF CPKAACSSSF FPTEQVSPTS240
LASLASQNOG SWTEKAVGSW APFFSFLCFL SFLPTLVSSS PCLGSGEVFT PEAWDMARGD300
FLFFFSPLRN SKWENTCFLR LGDFSVRLAG SVVSGSTCSS QRVLTPEFFF FFFFTRGISG360
```

ACPWATLLEG DVALKGETSA K

381

## (2) INFORMATION ON SEQ ID NO. 442:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 43 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

007335 12200

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

DHHNKLSQLQS QTYIILLSVN GEKISPYVLW VKCCNRLGLS NLP

43

(2) INFORMATION ON SEQ ID NO. 443:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 45 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

MVISIFPPLL YKLIFTHLLL YKLTFINTNK RLVLSQFICH EPRNN

45

(2) INFORMATION ON SEQ ID NO. 444:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 40 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GKPKNCCDEFF QGKLDNPNLL QHFTHKTYGL IFSPLTDSSI

40

(2) INFORMATION ON SEQ ID NO. 445:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 78 amino acids

007227 5622960



(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

GVGGGALRSA ALPWRTLPLT STCSRCTKPS TAEMEHLVQS WCLLNILMLQ THDFKWPLQR60  
 RSVNKS WNPL MMKCLQLI 78

(2) INFORMATION ON SEQ ID NO. 446:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 125 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

RLRRRGWRSP FGGAPMAHIT INQYLQQVYE AIDS RDGASC AELVSFKHPPH VANPRLQMAS 60  
 PEEKCQQVLE PPYDEMFAAH LRCTYAVGNH DFIEAYKCQT VIVQSFLRAF QAHKEENWAL120  
 LSCMQ 125

(2) INFORMATION ON SEQ ID NO. 447:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 80 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

004221 5652960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

MSCKHFIIRG FQDLLTLLW RGHLSWVCN MRMFKRHQLC TRCSISAVDG FVHLLQVLVN60  
GNVRHGSAAE RRAPPPTPQA 80

## (2) INFORMATION ON SEQ ID NO. 448:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 67 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

RSRGFSCVQT PCHFREVTA CVISLWQQVG GLPQGRRWPE MCFRSLTHHS LHTRREHHSW60  
SILRMEI 67

## (2) INFORMATION ON SEQ ID NO. 449:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 60 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

PITPYTHDVN TTPGAFSEWR FEFHVAASHT QTCHHSPHTH SRHSTAMSQK KFLVSDLKVL60

## (2) INFORMATION ON SEQ ID NO. 450:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 67 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

RATSGRSGFI KPSNLKQGTS FGSWLLNVVS GCVGNDGRFV CEKLPHGIQI SILRMLQEW60  
SRRVCRE

67

(2) INFORMATION ON SEQ ID NO. 451:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 111 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

SASHPESRLC RGGADMQAPR GTLVFALVIA LVPVGREPSS QGSQSALQTY ELGSENVKVP 60  
IFEEDTPSVM EIEMEELDKW MNSMNRNADF ECLPTLKEEK ESNHNPSDSE S 111

(2) INFORMATION ON SEQ ID NO. 452:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 51 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

EEWALEETAK GSCVYVDLKL IKFVSSSSSV GSLSRLPQGL LLENMSAIQ V

51

(2) INFORMATION ON SEQ ID NO. 453:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 59 amino acids

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(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

FDSFSSFKVG KHSKSAFLFM LFIHLSSSSI SISITEGVSS SKIGTFTFSL PSSYVCKAL 59

(2) INFORMATION ON SEQ ID NO. 454:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 107 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

PITTCSLGDP GKDKYTCTHR GRERCVRIC INILFSPDM RSQCCMMKRW YDSTYVPIVL 60  
 LFLYFLFRSF TIGRFQKHSF HHHLEMVCLN GDNSRSCSIS SRHGLLI 107

(2) INFORMATION ON SEQ ID NO. 455:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 73 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

RRGVSFLLSR QKWYHYVAAL QSPRARSLEN HLLSRFFFFL RVGVSLCCPK TRPGNCWGAK60  
 GIAPVPQASR VGR 73

004221"56557960

## (2) INFORMATION ON SEQ ID NO. 456:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

SWGNIIVRLLP SKKKKNAKEG DSLESELWEI GERQHNDTIS AYLEGKKLLS FSCMVTVISS60  
RKDISKE 67

## (2) INFORMATION ON SEQ ID NO. 457:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 81 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

DQPSLPFIRH KTLNLTSMAT KIIGSPETKW IDATSGIYNS EKSSNLSVTT DFSESLQSSN60  
IESKEINGIH DESNAFESKA S 81

## (2) INFORMATION ON SEQ ID NO. 458:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 41 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00/221"56EE/960

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

QLISPKAFRV LILNPKKSME FMMKAMLLNQ KHLESIFFEK P

41

(2) INFORMATION ON SEQ ID NO. 459:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 36 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

IPEVASIHFV SGEPILVAI LVRLRVLCRI NGREGW

36

(2) INFORMATION ON SEQ ID NO. 460:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 36 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

NSEGFRNQL LQIDLKIFLS CKFQKLHQST LFQVNL

36

(2) INFORMATION ON SEQ ID NO. 461:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 83 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

007227" 56E7960

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

GRRNDQLNLH IPQAGPFAGP YRLGWPLLSS GIRLPDWLVL HVSIKLKVIP WPPPGENQPH60  
 PASWGQWGRD FGLSEQLLEA AHD 83

(2) INFORMATION ON SEQ ID NO. 462:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

RRKASIIAFK GILLTLTQGV QSAREPILIS SSKMFLEENP WNVLKDVSGV RSSMWLAKGH60  
 LYLEQLEFIN SCSLVSLGAE VWHIFKPVHS RIQ 93

(2) INFORMATION ON SEQ ID NO. 463:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

TLNPHKTLISA KKARVIFFCI QDSTANLVFC YKNLVSHFLL KRTRITGTHP QLHETPSFLN60  
 EHESIYVHPS THMKMLCSST GMDGIRIKPI WKLKYF 96

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## (2) INFORMATION ON SEQ ID NO. 464:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

NLFTMKFLPE FSPFDTNMHH VSTFETQPNV ISVKSSLSLP SSNLPSPRVY LPFCAHLSYS60

SMLFYNCDSP GSLGAI

76

## (2) INFORMATION ON SEQ ID NO. 465:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

NQRMIEIYSN TKTERKCHST LKAANTIDHF IWLPSQESH NCKITCYCNS NVHKMAGKL 59

## (2) INFORMATION ON SEQ ID NO. 466:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN

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(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

HATVTQMCTK WQVNSRRRQI TAWKTQGRFY RNDIWLSELEG

40

(2) INFORMATION ON SEQ ID NO. 467:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 41 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

IPLQRFSLLT SLFFVLKLDL LVVHASLSLV TVNNLPTSSN Q

41

(2) INFORMATION ON SEQ ID NO. 468:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 65 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

LSKAIYFCKK AAACINHDHS STLNKERKRF LSLTQSLPLC HSPRGWGWT A HSKLTRLAIC60  
EYFSK

65

(2) INFORMATION ON SEQ ID NO. 469:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 56 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

PDWLFVNTTFP NKEGKGDVSY SGGKCSFSGK NGCRVGNQGS RCELLIRTGG KVVHSN 56

(2) INFORMATION ON SEQ ID NO. 470:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 109 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

ARPAPAGREG RGEGEATSRR CGVGHRA GPR EPAPHGAAV RPTPGPHHHC AALSGAENYR 60  
SRHAMKLASA LRRGPALHPL PPRANRGREP WRRRHRPRGW AAASRTWRS 109

(2) INFORMATION ON SEQ ID NO. 471:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 399 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

AAGACGARGS GRRGSYVPEV RCGAPGGAAG TGAPRSCCCQ TNPGPPSSLR RAFRRRELPF 60  
PACHEIGLGA EAGSGPPFPAP AARESRSRAM EEEASSPGLG CSKPHLEKLT LGITRILESS120  
PGVTEVTIIE KPPAERHMIS SWEQKNNCVM PEDVKNFYLM TNGFHM TWSV KLDEHIIPLG180  
SMAINSISKL TQLTQSSMYS LPNAPTADL EDDTHEASDD QPEKPHFDSR SVIFELDSCN240  
GSGKVCLVYK SGKPALAEDT EIWF LDRLY WHFLTDTFTA YYRLLITHLG LPQWQYAFTS300  
YGISPOAKQW FSMYKPITYN TNLLTEETDS FVNKLDPSKV FKSKNKIVIP KKKGPVQAPAG360  
GQKGPSGPGS PSTSSTSKSS SGSGETPPGK LRHPSFQFA 399

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## (2) INFORMATION ON SEQ ID NO. 472:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

RSAGGFSMMV TSVTPGEDSR MRVMPRVFS RCGLLQSPG DDASSMARD RDSRAAGAGG60  
 GDPASAPRP ISWHAGNGSS RRLKARRSDD GGPGLV 96

## (2) INFORMATION ON SEQ ID NO. 473:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

KYVSHANISI YKWRTLTL LLSYKIPNEVI ILSGITLYCK NASYFTFKFD NVCDEL 56

## (2) INFORMATION ON SEQ ID NO. 474:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

004227 5632960

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

WIFRVCCISR EIHFYILFY KHLDKGHLTH FKKHKCI

37

(2) INFORMATION ON SEQ ID NO. 475:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 33 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

PKGLSIKVRN NLDTRRKRCR LLNFIIHHIH CQI

33

(2) INFORMATION ON SEQ ID NO. 476:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 80 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

HIKIEFFGQN FWEAMHPTWA DIQPELFSRG EWYWQFMAEI HSDWLESMLY QLLNLSITL60  
AYCYYYISSI YRQKGFRNI

80

(2) INFORMATION ON SEQ ID NO. 477:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 48 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

00/22T" 5652960

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

SSLGKTFGKQ CILHGLIFSL SCSQEESGTG SLWLKSILIG WSLCYTSC

48

(2) INFORMATION ON SEQ ID NO. 478:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 70 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

EQLRLNISPC RMHCFPKVLP KELYFYVLSH RTGEKCSGHC WDLIFLGMGS GLMILATGVQ60  
ENGSPGSDSW 70

(2) INFORMATION ON SEQ ID NO. 479:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 400 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

PQQTWAVAG RWCNGPSLHR NRAGLDLPTI DTGYDSQPQD VLGIRQLERP LPLTSVCYPQ 60  
DLPRPLRSRE FPQFEPQRYF ACAQMLPPNL SPHAPWNYHY HCPGSPDHQV PYGHDYPRAA120  
YQQVIQPALP GQPLPGASVR GLHPVQKVIL NYPSPWDQEE RPAQRDCSFP GLPRHQDQPH180  
HQPPNRAGAP GESLECPAEL RPQVPQPPSP AAVPRPPSNP PARGLTKTSN LPEELRKVFI240  
TYSMDTAMEV VKFVNFLLVN GFQTAIDIFE DRIRGIDIK WMERYLRDKT VMIIVAISP300  
YKQDVEGAES QLDEDEHGLH TKYIHRMMQI EFIKQGSMMNF RFIPVLPNA KKEHVPTWLQ360

NTHVYSWPKN KKNILLRLLR EEEYVAPPRG PLPTLQVVPL

400

007221" 5667950

## (2) INFORMATION ON SEQ ID NO. 480:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 225 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

SSSGWRVARG SRHSSWGRR L GNLWSQLCRA LQGLPRSTSS IRWLVMWLVL VPWKPRKGAV 60  
 SLCGPLFLVP GAGIIQDNLL HRVQASHTGS RQGLPRQSRL DHLLVGCSRV VMALWHLVIG120  
 TSRTMVMIVP WSMWGKIGRQ HLCTCWIPLR FKLRELPGPE RSGEVLGVTH GGEGQGPFQL180  
 PDAQDILGLG IISRVYGWQI QACSVFVQAG AVAPSPCYRP RSLLR 225

## (2) INFORMATION ON SEQ ID NO. 481:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 125 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

KQRMQSSHRL HFKARVCGGL RGRALHNRFP GGQRASRGGT EKNQPGVLPT SLSQNAVRTR 60  
 PQTWPGLSDL GMNGVTREPP EGWAEAPVEE PHTLPLSAAA AGCFFYSWAS CRHECSEARW120  
 AHAPS 125

## (2) INFORMATION ON SEQ ID NO. 482:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 96 amino acids  
 (B) TYPE: Protein

00/227"56EE/960

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

VAMTAKDCSI MIALSPCLQD ASSDQRPVVP SSRSRFAFSV SVLDLCLKPY ESIPHQYKLD60  
GKIVNYYSKT VRAKDNVMS TRFKESEDCT LVLHKV 96

(2) INFORMATION ON SEQ ID NO. 483:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 66 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

LHCLPVCRMP ALIKGLWSLH RGPGLPFPCL CWTLTSSPTR AFPISINWTA RSSTIIQRLY60  
VPKTTT 66

(2) INFORMATION ON SEQ ID NO. 484:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 109 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

NKAFTIRES D MSPGWERRTI QNVFPGLNGH FHFKS VSSFL GHSTHFLHSL SRKFLVLFN 60  
SMSPRGNPTS KGVKSKNIHN QRSPNTTENI SIIQP SHYVQ VSKTLQGKS 109

002221 56552960

## (2) INFORMATION ON SEQ ID NO. 485:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 66 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

CSSIPCLQEA IPPQKGLKAK TFTTKGHPTQ QKISLSFSLH IMEKEQRHCR ERVRPCGELM60  
CNLRFP 66

## (2) INFORMATION ON SEQ ID NO. 486:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 109 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

ARPAPAGREG RGEGEATSRR CGVGHRAGPR EPAPHGAAAV RPTPGPHHHC AALSGAENYR 60  
SRHAMKLASA LRRGPALHPL PPRANRGREP WRRRHRPRGW AAASRTWRS 109

## (2) INFORMATION ON SEQ ID NO. 487:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 389 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```
AAGACGARGS GRRGSYVPEV RCGAPGGAAG TGAPRSCCCQ TNP GPPSSLR RAFRRREL PF 60
PACHEIGLGA EAGSGPPPAP AARESRSRAM EEEASSPGLG CSKPHLEKLT LGITRILESS120
PGVTEVTIIE KPPAERHMIS SWEQKNNCVM PEDVKNFYLM TNGFHM TWSV KLDEHI IPLG180
SMAINSISKL TQLTQSSMYS LPNAPTLADL EDDTHEASDD QPEKPHFDSR SVIFELDSCN240
GSGKVCLVYK SGKPALAEDT EIWF LD RALY WHFLTDTFTA YYRLLITHLG LPQWQYAFTS300
YGISPQAKQW FSMYKPITYN TNLLTEETDS FVNKLDP SKV FKSKNKIVIP KKKGPVQ PAG360
GQKGPSG PSG PSTSSTSKSS SGSGNPTRK 389
```

(2) INFORMATION ON SEQ ID NO. 488:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 96 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```
RSAGGF SMMV TSVTPGEDSR MRVMPRV SFS RCGLLQPS PG DDASSMARD RDSRAAGAGG60
GPD PASAPRP ISWHAGNGSS RRLKARRSDD GGPGLV 96
```

(2) INFORMATION ON SEQ ID NO. 489:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 152 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

```
LAAGRGKEEE MGFEDHGLPF LPLTHHTPPF PLSLSPLPKK KKKETFIMNQ QGFSPYQREM 60
WKELKKPPFV PNSTLPIFYA TQTLSEFVVF LQMDLLRRII VFHVFS PQVT KINICIYNLY120
YCYIFVDNTF RWCWVIYYNL NLGISFGLPQ SC 152
```

007227-5667960

## (2) INFORMATION ON SEQ ID NO. 490:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 91 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

GPWLTFPAFD PSHPISSSFP LPAAKKKKKG NVYHESTGFQ SLSKRDVERA KETTLCSQLH60  
FTHILCNTNT VLLGPFLTDG PLEKNYRIPR F 91

## (2) INFORMATION ON SEQ ID NO. 491:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 64 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

KWGTQRAGNF HYPILGLNLK EYIHYQELST KAGVKLHYTW LFTIPGSPPQ HDCGRPKDIP60  
RFRL 64

## (2) INFORMATION ON SEQ ID NO. 492:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 79 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

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(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

RFTASRVGNE PDINTPSSMP CPPSGPVFVK AGSHFSPQA VPKALEEPKE RQEPSWELTL60  
MTRGQLAQFP LFSWGEGTL 79

(2) INFORMATION ON SEQ ID NO. 493:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 100 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

KSSPDPARHY GSPPEGERRG KRSVPKVNPR SLGPTSLPTA TSHQPHARAR PFPLQLTAQQ 60  
MLGQNASPHL TKGLQPAGWE MNQILTPPPP CPAHLLGQYQ 100

(2) INFORMATION ON SEQ ID NO. 494:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 82 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

KGSLPPTKQG KLGQLAPGHQ GQLPTWLLPF LGFFQGFNS LGVGEVASCL HWYWPRRWAG60  
HGGGGVNIWF ISHPAGCKPL VK 82

007221 56E2960

## (2) INFORMATION ON SEQ ID NO. 495:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 79 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

RVPSPLNKG NWANWPLVIK VNSQLGSCLS LGSSRALGTA WGWEKWLPAF TGTGPEGGQG60  
MEEGVLISGS FPTLLAVNL 79

## (2) INFORMATION ON SEQ ID NO. 496:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 88 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

IQKVQYYTSP AAFVNGSLHS HWGTTVCMGR NSKCPHCGHW VGSAFCQGVC RNWLISVCQS60  
DQHTKVSAIK NVASLHPPSC YSGPSNLM 88

## (2) INFORMATION ON SEQ ID NO. 497:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 98 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

SHTSEKRRGT REEVTPASRS SISGVKRGTV ALPSWLRMRK SFLQWEEIHF SIPVQSDFMG60  
PVLNSDCIIN TIKRDSEMGs RIHWDNSKAY NTALMDPT 98

(2) INFORMATION ON SEQ ID NO. 498:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 83 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

AGYTPVSSTI RQLHQITGPR VTGWRMQGSH ILYGRDFGV LITLAYRNKPI PADSLTKGTP60  
HPMTTMRALA VSAHAHSCTP MAV 83

(2) INFORMATION ON SEQ ID NO. 499:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 85 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

GKICEYVNFL SLRDDRMFPY FSCKENNILT YTSCRKYHLE PLYYSTMFTL LYCQAESIKN60  
VHIHFELCIL FLKKGAGLWH WAGHD 85

004227 56337960

## (2) INFORMATION ON SEQ ID NO. 500:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 98 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

SYRLKGIGKC VFSRDHVESE QCWQTLPRKS CFSRCPCFGI SFLGRKKKSS LTIVNSISYF60  
SFCCSNGFPP TIIPSIYVLL YSPLSPVTFL SNTFPKFE 98

## (2) INFORMATION ON SEQ ID NO. 501:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 87 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

VSSCTSNHGV RSSLSSGEHK CTERDVLVRT TKELPSLSLT QAMCTCDAAE CAGVGGGHVA60  
PPEHFLTGKL GDPLLNVFVE IRTVSFT 87

## (2) INFORMATION ON SEQ ID NO. 502:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 53 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

TPKTLGCLLV SRVEQAQRES LGPELKEFIE PWQTGSKQPI LAAVLRRECG GQI

53

- (2) INFORMATION ON SEQ ID NO. 503:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

PSGPFSSLES TLLQVQAA IASFLSDCNS PIRFPCFYIC PPHSLNTAA RMGCLLPVCH60  
 GSINSLSSGP KDSRWACSTR DTSRQPSVLG V 91

- (2) INFORMATION ON SEQ ID NO. 504:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

VFIYDSLIIIP TSISSVHTVC QMFHAEPVSR ILLSDYGGFT TRPGSNSLGS KVGHSSMHR 59

- (2) INFORMATION ON SEQ ID NO. 505:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

DRKFWNQKID PVFSYIQSST SEFLFLNIGV LALFLKDALY LKRKLDERTG CGAVKYFRPR60  
SVYTFYRRNE VL 72

(2) INFORMATION ON SEQ ID NO. 506:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 102 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

SILGPGLCTH FIEEMKYSEV FWLPFHFCV LNLSHTYIV LLGAVVSFIK PLACVQKFLK 60  
GNTSNAYPLL ACYAACFTAI AVCFTVFKI PLSPFLVTGK AC 102

(2) INFORMATION ON SEQ ID NO. 507:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 68 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

NNEHKMLFII TSICEISYCK TTTGLLLNSL VIVFRLEMP TLVINITYN VFLGRHFIKC60  
IMPWLLLR 68

0073395.122700



## (2) INFORMATION ON SEQ ID NO. 508:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 65 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

LKFLQVLKFF FYSLHWIYVF LIPNMFNWDV CHSRAARQTF KSNSHTAELA FLLTQKFRKL60  
TVTVT 65

## (2) INFORMATION ON SEQ ID NO. 509:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 78 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

GPRAHWPLPN TMLEPKRANM GPEYNGDIFM FQPFNLTCLL LSFPPISSNL FCLTTYE/G66  
ITSSYRIPSS LMSCPQKY 78

## (2) INFORMATION ON SEQ ID NO. 510:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

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(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

SLKLLGFLDV ENTPCARHSI LYGSLGSVVA GFGHFLETSE YLYFLFLYVL KKAFLYIMNY60  
FFF 63

(2) INFORMATION ON SEQ ID NO. 511:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 53 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

SFVKWSPNLK LGNYEEKIA RYLLRSACRS AVGLVTIGSK VLLQWQILWP LSG 53

(2) INFORMATION ON SEQ ID NO. 512:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 43 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

ICCRACHHWK QGPTSVADLV AFEWLKTTTL HRAGAMHRHP SLP 43

(2) INFORMATION ON SEQ ID NO. 513:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 37 amino acids

00722T"56EEZ960

(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

QALQQIYRQT LTDTGQFSLL RNFLVLSWVT ILQNFTT

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(2) INFORMATION ON SEQ ID NO. 514:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 228 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

TGGARARRPL SAVARPARSS DPLRSAPLGP APPVNMIRCG LACERCRWIL PLLLLSAIAF 60  
 DIIALAGRGW LQSSDHGQTS SLWWKCSQEG GGSGSYEEGC QSLMEYAWGR AAAAMLFCGF120  
 IILVICFILS FFALCGPQML VFLRVIGLL ALAAVFQIIS LVIYPVKYTQ TFTLHANRAV180  
 TYIYNWAYGF GWAATIILIG CAFFFCCLPN YEDDLLGNAK PRYFYTSA 228

(2) INFORMATION ON SEQ ID NO. 515:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 94 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

DPLPPPSWEH FHHSEVDVWPW SLDCNQPRPA SAMMSKAMAL SRSRGRIQRQ RSQARPQRIM60  
 LTGGAGPSGA ERSGSEERAG RATAESGLRA RAPP 94

## (2) INFORMATION ON SEQ ID NO. 516:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 208 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

TLPKNGFKVA WRNSFFFWSP SQQQRFSPTE IPKLGRCEV PGLGIAQKVI FVVGEAEEEE 60  
 GTADQDNRCG PPKAVGPVID VSDSTVGMKG EGLGV LHGVN YQDDLEHSS QGKETS NHSQ120  
 EDKHLGSTEG EEGEDTDHQ DDEATEEHGS RCSTPRVLHE ALTALLVGPA AAALLGAFPP180  
 QRGRLAVVAR LQPAAAGQRD DVEGDGAE 208

## (2) INFORMATION ON SEQ ID NO. 517:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 204 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

PSCPPPEMKKE LPVDSCLP RS LELHPQKMDP KRQHIQLLSS LTECLTV DPL SASVWRQLYP 60  
 KHLSSQSSLL EHLSSWEQI PPKVQKSLQE TIQSLKLTNQ ELLRKGSSNN QDVVTCDMAC120  
 KGLLQVQGP RLPWTRLLLL LLVFAVGFLC HDLRSHSSFQ ASLTGRLLRS SGFLPASQQA180  
 CSKFTPTVCK VTGWLGEKCR FGV P 204

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(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 90 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

PEVMAQEAYS EDQQQQEEPR FGQPRTLNLL QQALAGHVTG DDILVVTATL PQQLLVGKLE60  
GLNGFLORLL YLLGNLLPGA EQVLQOKAGL 90

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 76 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

GTPKRHFSPN QPVTLQTVGV NLEHACWLAG KKPDDRSNRP VREAWKELCD RRSWHRKPTA60  
KTSSNRRSRV QGSRGP 76

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 355 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

FRHSMNGCEK DSSSTDSANE KPALIPREKK ISILEEPSKA LRGVTGPNIE KSVKDLQRCT 60  
VSLTRYRVMI KEEVDSSVKK IKAFAELHN CIIDKEVSLM AEMDKVKEEA MEILTARQKK120  
AEELKRLTDL ASQMAEMQLA ELRAEIKHFV SERKYDEELG KAARFSCDIE QLKAQIMLCG180  
EITHPKNNYS SRTPCSSLLP LLNAHAATSG KQSNFSRKSS THNKPSEGKA ANPKMVSSLP240  
STADPSHQTM PANKQNGSSN QRRRFNPQYH NNRLNGPAKS QGSGNEAEPL GKGNSRHEHR300  
RQPHNGFRPK NKGGAKNQEA SLGMKTPEAP AHSEKPRRRQ ARCRTPREGQ GPFRG 355

(2) INFORMATION ON SEQ ID NO. 521:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 120 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

NQNVKNRGTO KKCLPSVEKL PNPPWGQKNA TVKTPNRKLT PERPLALPRC PAACLPSPGL 60  
FRMGRGLGGL HPQGSLLIFG TAFVFGPEAV VRLSSVFVAA VALSQWLGI PTALRLGRPI120

(2) INFORMATION ON SEQ ID NO. 522:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 116 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

RAVRISMASS LTLISASINE TSLSMQLCN SAKAALIFFT ELSTSSLIMT RYLVRETVQR 60  
CKSFTDFSIF GPVTPRSAFE GSSSIEIFFS RGIRAGFLA ESVDLSFSQ PFMLCR 116

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## (2) INFORMATION ON SEQ ID NO. 523:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 130 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

RRQRKAEPGA CALGRVGSEC IPEPGARRTA QAAGLRVSG AANTKVRELK HFRFLGLLRS 60  
CRSEMEVDAP GVDGRDGLRE RRGFSEGGRO NFDVRPQSGA NGLPKHSYWL DLWLFILEFDV120  
VVFLFVYFLP 130

## (2) INFORMATION ON SEQ ID NO. 524:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 78 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

ISANKSWQKI HKEKHHHIEK DEKPEVQPVG VFGKPICPRL RPHIEVLPPS LAKASPLPET60  
ISTINTRCVH LHLAPAAS 78

## (2) INFORMATION ON SEQ ID NO. 525:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 95 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

GLTSKFCLPP SLKPRRSRRP SRPSTPGAST SISLLQLRNN PRNRKCLSSR TLVFAAPETE60  
RSPAACAVRR APGSGMHSEP TLPSAQAPGS AFRCL 95

(2) INFORMATION ON SEQ ID NO. 526:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 112 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

SLNSTFSVLP QKFPQFQHR AVYNSFSFPG QAARYPWMAF PRNSIMHLNH TANPTSNSNF 60  
LDLNLPPQHN TGLGGIPVAG EEEVKVSTMP LSTSSHSLQQ GQQTSLHTT VA 112

(2) INFORMATION ON SEQ ID NO. 527:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 72 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

RFRPCHCQPL PIHYNKDSSL QVSTLLWPDN RTERRGLDSG VLAWATGFLH DSFMILLMY60  
TPRRANINV HA 72

(2) INFORMATION ON SEQ ID NO. 528:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 102 amino acids

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(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

RNHAKIQLPM QAPQSLILSS QFCCQATVVW RLVGCCPCCN EWEEVDSGMV ETFTSSSPAT 60  
GIPPRPVLCC GGRFKSKLL FEVGFAVWFK CMMLLRGKAI QG 102

(2) INFORMATION ON SEQ ID NO. 531:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1708 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

```

CCTGGAAACA AGATCCAAAC CCAAGTGACC CCGCCGGAAA GTGACCCAGT CAGGTTTAAA 60
AATTCCAACA AACCGACGTG AACAAATAGA CCGACCAACC AAATATACAA TCCGTCAAAA 120
TACATTCACT TCCACTACGA AACCCCAACA AAGGGTGTGA ATGCCCCCCC AGGAGAGACG 180
GTTTTGGTTT CATCAAGTGT GTGGATCGTG ATGTTCTGTAT GTTCTTCCAC TTCAGTGAAA 240
TTCTGGATGG GAACCGAGCTC CATATTGCAG ATGAAGTAGA GTTTACTGTG GTTCCTGATA 300
TGCTCTCTGC TCAAAGAAAT CATGCTATTA GGATTAAAAA ACTTCCCAAG GGCACGGTTT 360
CATTTTCATT CCATTTCAGAT CACCGTTTTT TGGGCACGGT AGAAAAAGAA GCCACTTTTT 420
CCAATCCTAA AACCACTAGC CCAAATAAAG GCAAAGAGAA GGAGGCTGAG GATGGCATT 480
TTGCTTATGA TGA CTGTGGG GTGAAACTGA CTATTGCTTT TCAAGCCAAG GATGTGGAAG 540
GATCTACTTC TCCTCAAATA GGAGATAAGG TTGAATTTAG TATTAGTGAC AAACAGAGGC 600
CTGGACAGCA GGTGTGCAACT TGTGTGCGAC TTTTAGGTCG TAATTCTAAC TCCAAGAGGC 660
TCTTGGGTTA TGTGGCAACT CTGAAGGATA ATTTTGGATT TATTGAAACA GCCAATCATG 720
ATAAGGAAAT CTTTTTCCAT TACAGTGAGT TCTCTGGTGA TGTTGATAGC CTGGAAC TGG 780
GGGACATGGT CGAGTATAGC TTGTCCAAAG GCAAAGGCAA CAAAGTCAGT GCAGAAAAAG 840
TGAACAAAAC ACACTCAGTG AATGGCATT  CTGAGGAAGC TGATCCCACC ATTTACTCTG 900
GCAAAGTAAT TCGCCCCCTG AGGAGTGTTG ATCCAACACA GACTGAGTAC CAAGGAATGA 960
TTGAGATTGT GGAGGAGGGC GATATGAAAG GTGAGGTCTA TCCATTTGGC ATCGTTGGGA1020
TGGCCAACAA AGGGGATTGC CTGCAGAAAG GGGAGAGCGT CAAGTTCCAA TTGTGTGTCC1080
TGGGCCAAAA TGCACAAACT ATGGCTTACA ACATCACACC CCTGCGCAGG GCCACAGTGG1140
AATGTGTGAA AGATCAGTTT GGCTTCATTA ACTATGAAGT AGGAGATAGC AAGAAGCTCT1200
TTTTCCATGT GAAAGAAGTT CAGGATGGCA TTGAGCTACA GGCAGGAGAT GAGGTGGAGT1260
TCTCAGTGAT TCTTAATCAG CGCACTGGCA AGTGCAGCGC CTGTAATGTT TGGCGAGTCT1320
GTGAGGGCCC CAAGGCTGTT GCAGCTCCTC GACCTGATCG GTTGGTCAAT CGCTTGAAGA1380
ATATCACTCT GGATGATGCC AGTGCTCCTC GCCTAATGGT TCTTCGTCAG CCAAGGGGAC1440
CAGATAACTC AATGGGGTTT GGTGCAGAAA GAAAGATCCG TCAAGCTGGT GTCATTGACT1500
AACCACATCC ACAAAGCACA CCATTAATCC ACTATGATCA AGTTGGGGGG AATCTGGTGA1560
AGGGTTCTGA ATATCTCCCT CTTTCATCCCT CCCGAAATCT GGAATACTTA TTCTATTGAG1620
CTATTACACC AGTTTTAACA CCTTCCTCGT GTTATGTTTA AAAAAATAAA TAAATTTAAG1680
AAAACCATT TAAATAATGA AAAGTTGG

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## (2) INFORMATION ON SEQ ID NO. 532:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2128 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

CTGTATCCTA ATTTCTTGGT GAATGAACTC ATTCTTAAAC AGAAGCAAAG ATTTGAGGAA 60  
 AAGAGGTTCA AATTGGACCA CTCAGTGAGT AGCACCAATG GCCACAGGTG GCAGATATTT 120  
 CAAGATTGGT TGGGAACTGA CCAAGATAAC CTTGATTTGG CCAATGTCAA TCTTATGTTG 180  
 GAGTTACTAG TGCAGAAGAA GAAACAACCTG GAAGCAGAAT CACATGCAGC CCAACTACAG 240  
 ATTCTTATGG AATTCCTCAA GGTTGCAAGA AGAAATAAGA GAGAGCAACT GGAACAGATC 300  
 CAGAAGGAGC TAAGTGTTTT GGAAGAGGAT ATTAAGAGAG TGGAAGAAAT GAGTGGCTTA 360  
  
 TACTCTCCTG TCAGTGAGGA TAGCACAGTG CCTCAATTTG AAGCTCCTTC TCCATCACAC 420  
 AGTAGTATTA TTGATTCCAC AGAATACAGC CAACCTCCAG GTTTCAGTGG CAGTTCTCAG 480  
 ACAAAGAAAC AGCCTTGGTA TAATAGCAGC TTAGCATCAA GACGAAAACG ACTTACTGCT 540  
 CATTTTGAAG ACTTGAGCA GTGTTACTTT TCTACAAGGA TGTCTCGTAT CTCAGATGAC 600  
 AGTCGAACTG CAAGCCAGTT GGATGAATTT CAGGAATGCT TGTCCAAGTT TACTCGATAT 660  
 AATTCACTAC GACCTTTAGC CACATTGTCA TATGCTAGTG ATCTCTATAA TGGTTCCAGT 720  
 ATAGTCTCTA GTATTGAATT TGACCGGGAT TGTGACTATT TTGCGATTGC TGGAGTTACA 780  
 AAGAAGATTA AAGTCTATGA ATATGACACT GTCATCCAGG ATGCAGTGGA TATTCATTAC 840  
 CCTGAGAATG AAATGACCTG CAATTCGAAA ATCAGCTGTA TCAGTTGGAG TAGTTACCAT 900  
 AAGAACCTGT TAGCTAGCAG TGATTATGAA GGCACGTGTA TTTTATGGGA TGGATTACA 960  
 GGACAGAGGT CAAAGGTCTA TCAGGAGCAT GAGAAGAGGT GTTGGAGTGT TGACTTTAAT1020  
 TTGATGGATC CTAAACTCTT GGCTTCAGGT TCTGATGATG CAAAAGTGAA GCTGTGGTCT1080  
 ACCAATCTAG ACAACTCAGT GGCAAGCATT GAGGCAAAGG CTAATGTGTG CTGTGTTAAA1140  
 TTCAGCCCCCT CTTCCAGATA CCATTTGGCT TTCGGCTGTG CAGATCACTG TGTCCACTAC1200  
 TATGATCTTC GTAACACTAA ACAGCCAATC ATGGTATTCA AAGGACACCG TAAAGCAGTC1260  
 TCTTATGCAA AGTTTGTGAG TGGTGAGGAA ATTGTCTCTG CCTCAACAGA CAGTCAGCTA1320  
 AAAGTGTGGA ATGTAGGGAA ACCATACTGC CTACGTTCTT TCAAGGGTCA TATCAATGAA1380  
 AAAAAGCTTTG TAGGCCTGGC TTCCAATGGA GATTATATAG CTTGTGGAAG TGAATAAAC1440  
 TCTCTCTACC TGTACTATAA AGGACTTTCT AAGACTTTGC TAACTTTTAA GTTTGATACA1500  
 GTCAAAAGTG TTCTCGACAA AGACCGAAAA GAAGATGATA CAAATGAATT TGTTAGTGCT1560  
 GTGTGCTGGA GGGCACTACC AGATGGGGAG TCCAATGTGC TGATTGCTGC TAACAGTCAG1620  
 GGTACAATTA AGGTGCTAGA ATTGGTATGA AGGGTTAACT CAAGTCAAAT TGTACTTGAT1680  
 CCTGCTGAAA TACATCTGCA GCTGACAATG AGAGAAGAAA CAGAAAATGT CATGTGATGT1740  
 CTCTCCCCAA AGTCATCATG GGTTTGGAT TTGTTTGGAA TATTTTTTTC TTTTTTCTT1800  
 TTCCCTCCTT TATGACCTTT GGGACATTGG GAATACCCAG CCAACTCTCC ACCATCAATG1860  
 TAACTCCATG GACATTGCTG CTCTTGGTGG TGTTATCTAA TTTTGTGAT AGGGAAACAA1920  
 ATTCTTTTGA ATAAAAATAA ATAACAAAAC AATAAAAAGT TATTGAGCCA CAAAAAAA1980  
 AAAAAAAAAA AAAAAAAAAA ACAAAGAGA AAACAAAGGT TACGAAGTAG CATATGTGAA2040  
 CTATAATGTA ACAGTGAATA ATTTGTAAAG TTCGTATTTT CCAACCTCTT TGGGAATTAC2100  
 ACATATCAAT ATAAACAAAA TATAAGT 2128

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## (2) INFORMATION ON SEQ ID NO. 533:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2640 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

CTAGCAAGCA GGTAACGAG CTTTGTACAA ACACACACAG ACCAACACAT CCGGGGATGG 60  
 CTGTGTGTTG CTAGAGCAGA GGCTGATTAA ACACTCAGTG TGTGGCTCT CTGTGCCACT 120  
 CCTGGAAAAAT AATGAATTGG GTAAGGAACA GTTAATAAGA AAATGTGCCT TGCTAACTGT 180  
 GCACATTACA ACAAAGAGCT GGCAGCTCCT GAAGGAAAAG GGCTTGTGCC GCTGCCGTTT 240  
 AAACCTTGTC GTCAACTCAT GCCAGCAGCC TCAGCGTCTG CCTCCCCAGC ACACCCTCAT 300  
 TACATGTGTC TGTCTGGCCT GATCTGTGCA TCTGCTCGGA GACGCTCCTG ACAAGTCGGG 360  
 AATTTCTCTA TTTCTCCACT GGTGCAAGA GCGGATTTCT CCCTGCTTCT CTTCTGTAC 420  
 CCCCCTCCT CTCCCCCAGG AGGCTCCTTG ATTTATGGTA GCTTTGGACT TGCTTCCCG 480  
 TCTGACTGTC CTTGACTTCT AGAATGGAAG AAGCTGAGCT GGTGAAGGGA AGACTCCAGG 540  
 CCATCACAGA TAAAAGAAAA ATACAGGAAG AAATCTCACA GAAGCGTCTG AAAATAGAGG 600  
 AAGACAACT AAAGCACCAG CATTGAAGA AAAAGGCCCT GAGGGAGAAA TGGCTTCTAG 660  
 ATTGAATCAG CAGCGGAAAA GAACAGGAAG AGATGAAGAA GCAAAATCAA CAAGACCAGC 720  
 ACCAGATCCA GGTCTAGAA CAAAGTATCC TCAGGCTTGA GAAAGAGATC CAAGATCTTG 780  
 AAAAAGCTGA ACTGCAATC TCAACGAAGG AAGAGGCCAT TTTAAAGAAA CTAAAGTCAA 840  
 TTGAGCGGAC AACAGAAGAC ATTATAAGAT CTGTGAAAGT GGAAAGAGAA GAAAGAGCAG 900  
 AAGAGTCAAT TGAGGACATC TATGCTAATA TCCCTGACCT TCCAAAGTCC TACATACCTT 960  
 CTAGGTTAAG GAAGGAGATA AATGAAGAAA AAGAAGATGA TGAACAAAAT AGGAAAGCTT 1020  
 TATATGCCAT GGAAATTTAA GTTGAAAAAG ACTTGAAGAC TGGAGAAAGT ACAGTTCTGT 1080  
 CTTCCAATAC CTCTGGCCAT CAGATGACTT TAAAGGTAC AGGAGTAAAA GTTTAAGATG 1140  
 ATGGGCAAAA GTCCAGTGTA TTCAGTAAAG TGCTAATCAC AAGTTGGAGG TCAATGGCAC 1200  
 CGATGGCCTG GCACCAAGTTG AAGTAGAGGA ACTTCTAAGA CAAGCCTCAG AGAGAACTC 1260  
 TAAATCCCCA ACAGAGTATC ATGAGCCTGT ATATGCCAAT CCCTTTTACA GGCCTACAAC 1320  
 CCCACAGAGA GAAACGGTGA CCCCTGGACC AAACCTTTCAA GAAAGGATAA AGATTTAAAC 1380  
 TAATGGACTG GGTATTGGTG TAAATGAATC CATAACAAT ATGGGCAATG GTCTTTTACA 1440  
 GGAAAGGGGA AACAACCTCA ATCACATCAG TCCCATTCCG CCAGTGCCTC ATCCCGATC 1500  
 AGTGATTCAA CAAGCAGAAG AGAAGCTTCA CACCCCGCAA AAAAGGCTAA TGACTCCTG 1560  
 GGAAGAATCG AATGTCATGC AGGACAAAGA TGCACCTCT TCACCCACTT GTCAGGAGGA 1620  
 CAGAGAGACA ATATTTGGGA AATCTGAACA CCAGAATTCT TCACCCACTT GTCAGGAGGA 1680  
 CGAGGAAGAT GTCAGATATA ATATCGTTCA TTCCCTGCCT CCAGACATAA ATGATACAGA 1740  
 ACCGGTGACA ATGATTTTCA TGGGGTATCA GCAGGCAGAA GACAGTGAAG AAGATAAGAA 1800  
 GTTTCTGACA GGATATGATG GGATCATCCA TGCTGAGCTG GTTGTGATTG ATGATGAGGA 1860  
 GGAGGAGGAT GAAGGAGAAG CAGAGAAACC GTCCTACCAC CCCATAGCTC CCCATAGTCA 1920  
 GGTGTACCAG CCAGCCAAAC CAACACCACT TCCTAGAAAA AGATCAGAAG CTAGTCCTCA 1980  
 TGAAAACACA AATCATAAAT CCCCCACAA AAATTCATA TCTCTGAAAG AGCAAGAAGA 2040  
 AAGCTTAGGC AGCCCTGTCC ACCATTCCCC ATTTGATGCT CAGACAACTG GAGATGGGAC 2100  
 TGAGGATCCA TCCTTAACAG CTTTAAGGAT GAGAATGGCA AAGCTGGGAA AAAAGGTGAT 2160  
 CTAAGAGTTG TACCACCTAT ATAAACATCC TTTGAAGAAG AAACCTAAGAA GCATTTGCAA 2220  
 ATTTCTCTTC TGGATATTTT GTTTATTTT TCTGAAGTCC AAAAAATTAT CATTACAGTG 2280  
 TACCATATTA AGCCATGTGA ATAAGTAGTA GTCATTATTT GTGAAAAATT CCCAAAAGC 2340  
 TGGGGAAAAA AAATGTGTAA CTTTTCCAGT TACTTGACAC GATTCAAGTG GGGAAAACCA 2400  
 GCATTTTTTA TTCTATTGAT ACCAAAGCAT TTCTAATAAG AGCTTGTTAA ATTTAAGAAT 2460  
 AAAGTTATTT AAAATATTCT GAGTATAGTA TATTAAGTGG CATTGTAATT TTGATGATAC 2520  
 AAAGATTGAA AGATCATAGG AAAGCATTGC CCTTCATCAC AGAAGTATTC AACTCTGACA 2580  
 AATAAATATG TCATCCTGAA TTAATAATGC CTTAATAAAA GTACATCCTC CTGCTAAAAA 2640

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## (2) INFORMATION ON SEQ ID NO. 534:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1245 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

```

TGCAGCGCGT GCGTGCTGCG CTA CTGAGCA GCGCCATGGA GGACTCTGAA GCACTGGGCT 60
TCGAACACAT GGGCCTCGAT CCCC GGCTCC TTCAGGCTGT CACCGATCTG GGCTGGTTCG 120
GACCTACGCT GATCCAGGAG AAGGCCATCC CACTGGCCCT AGAAGGGAAG GACCTCCTGG 180
CTCGGGCCCC CACGGGCTCC GGG AAGACGG CCGCTTATGC TATTCCGATG CTGCAGCTGT 240
TGCTCCATAG GAAGGCGACA GGTCCGGTGG TAGAACAGGC AGTGAGAGGC CTTGTTCTTG 300
TTCCTACCAA GGAGCTGGCA CGGCAAGCAC AGTCCATGAT TCAGCAGCTG GCTACCTACT 360
GTGCTCGGGA TGTCCGAGTG GCCAATGTCT CAGCTGCTGA AGACTCAGTC TCTCAGAGAG 420
CTGTGCTGAT GGAGAAGCCA GATGTGGTAG TAGGGACCCC ATCTCGCATA TTAAGCCACT 480
TGCAGCAAGA CAGCCTGAAA CTTCTGACT CCCTGGAGCT TTTGGTGGTG GACGAAGCTG 540
ACCTTCTTTT TTCCTTTGGC TTTGAAGAAG AGCTCAAGAG TCTCCTCTAG TCACTTGCCC 600
CGGATTTACC AGGCTTTTCT CATGTCAGCT ACTTTTAACG AGGACGTACA AGCACTCAAG 660
GAGCTGATAT TACATAACCC GGTTACCCTT AAGTTACAGG AGTCCCAGCT GCCTGGGCCA 720
GACCAGTTAC AGCAGTTTCA GGTGGTCTGT GAGACTGAGG AAGACAAATT CCTCCTGCTG 780
TATGCCCTGC TCAAGCTGTC ATTGATTCTG GGCAAGTCTC TGCTCTTTGT CAACACTCTA 840
GAACGGAGTT ACCGGCTACG CCTGTTCTTG GAACAGTTCA GCATCCCCAC CTGTGTGCTC 900
AATGGAGAGC TTCCACTGCG CTCCAGGTGC CACATCATCT CACAGTTCAA CCAAGGCTTC 960
TACGACTGTG TCATAGCAAC TGATGCTGAA GTCCTGGGGG CCCCACGTCA ACGGGCAATG1020
CGACCCCGGC GACGAGCCAA AACGGGGACA ATGGCCTCTC GATTCTGGA ACGCACGGTC1080
GTGGCCCTGG GGCCTAGAC CTTCCACCAT CGTGTCTGCA TGTGCTCAAC TTTTGATCTT1140
CCCCCCCCAAC CCCTGAGGCC TAACATCCAT CGAGCTTGGC AGGACAGCAA CGCGCTAACA1200
ACCCAGGGCA TAGGTCTTAA CCTTTGGTGC TTTCCACGG AGGCG 1245

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09673395.122700

## (2) INFORMATION ON SEQ ID NO. 535:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 822 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

AAGATCGGTC TTTGTCCTTA TCCTTATCCT TATTCTAATG GCAGTTAGAT GCNNTTCTTT 60  
 AGAGGGGGCA ATGAGACAGC CAGGTGGGAA GGGGTCCCCA GAGAACTCC AGCCTGCACA120  
 CTGGGAGGAG TGTGCACTGG GGTGAAGCCA CCGGAAGTTT GCGCCATCTC CAGTGGGGAA180  
 GAGCCCAGCC CCTCCTCTTC CTGGGTGGGA AACTGCGATT CAAACTGCCA GGTGGGAAGT240  
 CCATGGGCAG GAAACAGGCT CTCGNTTTC TAAGAGTCTC TGTTTCCCCC TTTTTCCTT300  
 TATGCCTAAT TAATAAATTC CATTTTCTC ACCCTTCAA CAGCCTGTGA GCCTAAATTT360  
 TTGTGGCCAT GGGACAGACA AGGACCCCGT CTTAGCTGA ACTAAGGAGA AAGTCCCCAA420  
 ACAATGGGAA GAAAGGCAGG GAGTAGACAT CCAATTTCTT GCGGTGGATT GTGAGGGGT480  
 ACCATGGTTC TGACCAGATG TGTATCAGGA GCTGTGTTGC AGGAAGTCTC AGGAATGAAG540  
 TTGATAGCTT TCTTCCATC ACATGATGAC TGAAAAGACG AAGGCATCTA ATGAGTTAGA600  
 GTCACACCAT CTCATGCCTG TATACTATCA AACAACTTTT GGAAGCTAG CCTTGTTGG660  
 GAAAACATCA TTTCTTAACT GAATGCCTGG ATGCAAGCAA AGTCTCATTC TTGATCATGA720  
 TGAGGTTTAC CATGTCTTCT TGACAGGATC CTGCAAACAA ACCCACAATT GCTACTATGA780  
 CATGCAACTC CATGGTTAAT TCCTTGATA GCAAATAGCT CG 822

## (2) INFORMATION ON SEQ ID NO. 536:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2703 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

09673395 "122700



(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

AGTTCGGCAC AGGGGGAGGA ACCTGGCCCT GGGAGGAGGC TGTTCGTGC TCCTAGAGAA 60  
TCCCGTTCTG AAGGGAAGAG CATGTTTGC GCGTCCCCA CCATGCGTGA GAGCTCCCC 120  
AAACAGTACA TGCAGCTCGG AGGCAGGGTC TTGCTGGTTC TGATGTTTCA GACCCTCCTT 180  
CACTTTGACG CCAGCTTCTT TTCTATTGTC CAGAACATCG TGGNGCACAN GCTCTGATGA 240  
TTTTNAGTGG CCATTGGTTT TAAAACCAAG CTGGCTGCTT TGACTCTTGT TGTGTGGCTC 300  
TTTGCCATCA ACGTATATTT CAACGCCTTC TGGACCATTC CAGTCTACAA NGCCCATGCA 360  
TGACTTCCNT GAAATACGAC NTTCTTCCAG ACCATGTCGG TGATTGGGGG CTTGCTCCTG 420  
GNTGGNTGGC CCTGGGCCCT NGGGGGTGTC TCCATGGATG AGAAGAAGAA GGAGTGGTAA 480  
CAGTCACAGA TCCCTACCTG CCTGGCNTNA AGACCCNGTN GGCCGTCAAG GNACTGGNTT 540  
CNGGGGTGGA TTCAACNAAA ANCTGNCCAG CTTTNNATGT ATCCTCTTCC CTTCCCCTCC 600  
CTTGGTAAAG GCACAGATGT TTTGAGAANC TTTATTGCA GAGACACCTG AGAATNCGAT 660  
GGNCTCAGTC TGCTCTGGAG CCACAGTCTG GCGTCTGACC CTTCAGTNGC AGGCCNAGCC 720  
TGGCANGCTG GNAAGCCNTC CCCCACGCC GAGGCTTTNG GNAGTGAANC AGNCCCGCTT 780  
NGGNCTGTGG CATCNTCAGT CCNTATTTTT GAGTTTTTTT GTGGGGGTAN NCAGGAGGGG 840  
GCCTTCAAGC TGTACTGTGA NGCAGACGCA NTTGGTATTA TCATTCAAAG CAGTCTCCCT 900  
CTTNATTTGT AAGTTTNACA TTTTNNAGC GGAACTACT AAATTATTTT GGGNTGGTTC 960  
AGCCAAACCT CAAAACAGTT AATCTCCNT GGNTTTNAAA ATCACACCAG TGGNCTTTNG 1020  
ATGTTGTTTC TGCCCCGCAT TNGTATTTTA TAGGNNAAATA GTGAAAACAT TTAGGGNACA 1080  
CCCAANAGAA TGATNGCAGT ATTAAAGGGG TGGTAGAAGC TGCTGTTTAT GATAAAAGTC 1140  
ATCGGTGAGA AAATCAGCTT GGATTNGGT CCAAGTGNNN TTTATTGGG TAACACCCTG 1200  
GGAGTTTTAG TAGCTTGAGG CAAGGTGGAG GGGCAAGAAG TCCTTGGGGA AGCTCTGGT 1260  
CTGGGTNGCT NGCTGGCCTC CAAGCTGGCA GTGGGAAGGG CTAGTGNAGA CCACANGG 1320  
GGTAGCCCN AGCAGCAGCA CCCTGCAANG CCAGCCNTGG CCNAGCTNNG CTCNAGACCA 1380  
GCNTTNGCAG ANGCCGCAGN CCGCTGTNNG GGCANGGGGG TGTNGGCAGG AGCTCCCNAG 1440  
CACTNGGNAG ACCCAGCGAC NTCAACCCAG TTNACCTCAC ATGGGGCCNT TTTCTGAGC 1500  
AAGGTCTNCG AAAGCGCAGG CCGCCCTGGN CTGAGCAGCA CCGCCCTTTC CCAGCTGCAC 1560  
TCGCCCTGTG GACAGCCCCG ACACACCANC TTTCTNGAG GCTGTCGCTC ACTCAGATTG 1620  
TCCGTTTGCT ATGCCGAATG CAGCCAAAAN TTCCTTTTTA CAATTTGTGA TGCCTTACCG 1680  
ATTTGATCTT AATCCTGTAT TTAAAGTTTT CTAACACTGN NCCTTAAACT GTGTTTCTCT 1740  
TTTTGGGGGA GCTTAACTGC TTGTTGCTCC CTGTGCTCTN GCACCATAGT AAATGCCACA 1800  
AGGGTAGTCG AACACCTCTC TGGCCCCTAG ACCTATCTGG GGACAGGCTG GCTCAGNCTG 1860  
TCTNCCANGG GCTGCTGCGG CCCAGCCCCG AGCCTGCCTC CCTCTTGGNC CTCTCATCCA 1920  
TTGGNCTCTG CAGGGCANGG GGTGAGGCAG GTTCTNNGCN TCATAAGTGC TTTTNGGAAG 1980  
TCACCTACCT TTTTAACACA GCCGAACTAN GTCCCAACGC GNTTTGCAA TATCCCCTN 2040  
GGTAGCCTAC TTNCCTTANC CCCCGAANTA TTGGTAAGAT CGAGCAATGG NNCTTCAGGA 2100  
NCATNGGGTT CTCTTCTCCT GTGATCATTN CAAGTGCTCA CTGCNATNGA ANGACTNGGC 2160  
TTGNTCNTCA GTGTTTCNAA CCTNACCAG GGCNTGTCTC TTGGTCCACN ACCTCGCTCC 2220  
CTGTTAGTGC CGTATGACAG CCCCNATCN AAATGACCTT GGCCNAAGTN CACNGGTTTC 2280  
TCTGTGGTNC AAGGTGGT GGTGATTGG TGGAANGTN AGGGTGNGAC CNAAANGGAG 2340  
GNCCACGTGA NGCAGNTCNA GCACCANNGT TNCTGCANCC AGCAGCNGCC TCCGTNCTA 2400  
GTGGGTGTTN CCTNGTTTN TNCCTGGCCC NTGGGTNGGG CTNAGGGNCC TGATTGGGN 2460  
AANGATGCCT TTGNACANGG AGGGGAGGAN TAAGTGGGAT CTACCNAANT TNGATTCTGG 2520  
CAAAACAANT TTCTAAGANT TTTTTGCTT TATGTGGGNA AACAGATCTA AATCTCATTT 2580  
TATGCTGTAT TTTATATCNT TNAGTTGTGT TTGAAAACNG TTTNTGATTT TTGGAAACAC 2640  
ATCAAAATAA ATAATGGCGT TTGTTGTAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2700  
AAA

2703

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 537:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2664 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

CTCCCAGGGA GTGCTGAGTA GTGATGGTGT CTGGAGGGTC AAATCCATTC CCAATGGCAA 60  
 AGGTTCTCA CCACTCCCCA CCGCTACAAC TCCAAAACCA CTTATCCCTA CAGAGGCCAG 120  
 CATCAGGGTC TGGGGCACGA GCGGCACGAG CCATCTCCAT CCCCAGGACA TCTGTATGAT 180  
 TCAGAAGTAC AACCACGATG GGAAGCAGG TCGGCTGGAG GCTTTTAGCC AAGGGGAAAG 240  
 TGTCTTAAAG GAACCCAAGT ACCAGGAAGA GCTGGAGGAC AGGCTGCATT TCTACGTGGA 300  
 GGAATGTGAC TACTTGACAG GCTTCCAGAT CCTGTGTGAC CTGCACGATG GCTTCTCTGG 360  
 GGTAGGCGCG AAGGCGGCAG AGCTGCTACA AGATGAATAT TCAGGGCGGG GAATAATAAC 420  
 CTGGGGCCTG CTACCTGGTC CCTACCATCG TGGGGAGGCC CAGAGAAACA TCTATCGTCT 480  
 ATTAACACA GCTTTTGGTC TCGTGCACCT GACTGCTCAC AGCTCTCTTG TCTGCCCCCT 540  
 GTCCTTGGGT GGGAGCCTGG GCCTGCGACC CGAGCCACCT GTCAGCTTCC CTTACCTGCA 600  
 TTATGATGCC ACTCTGCCCT TCCACTGCAG TGCCATCCTG GCTACAGCCC TGGACACAGT 660  
 CACTGTTCTT TATCGCCTGT GTTCTCTCC AGTTTCCATG GTTCATCTGG CTGACATGCT 720  
 GAGCTTCTGT GGGAAAAGG TGGTGACAGC AGGAGCAATC ATCCCTTTCC CTTGGCTCC 780  
 AGGCCAGTCC CTTCTGATT CCCTGATGCA GTTTGGAGGA GCCACCCCAT GGACCCACT 840  
 GTCTGCATGT GGGGAGCCTT CTGGAACACG TTGCTTTGCC CAGTCAGTGG TGCTGAGGGG 900  
 GTATAGACAG AGCATGCCAC ACAAGCCACA GAACCAAAGG GACACCTCCA CCCTCTGCCC 960  
 TTCATGCATG TACCACTGGG GAAGAAATCT TGGCTCAGTA TTTACAACAG CAGCAGCCTG 1020  
 GAGTCATGAG TTCTTCCCAT CTGCTGCTGA CTCCCTGCAG GGTGGCTCCT CTTACCCCC 1080  
 ACCTCTTCTC AAGCTGCAGT CCACCGGTA TGGTCTGGA TGGTCCCCC AAGGGAGCAG 1140  
 GTCCTCTGTT TCCCTCTCCC TTCCACAGCA GTGGAGAGCA TCCCAGTGTT TGGGGCACTG 1200  
 TGTTCTCTT CGTCCCTGCA CCAGACCCTG GAAGCCTTGG CCAGAGACCT CACCAAACCT 1260  
 GACTTGCGGC GCTGGGCCAG CTTTATGGAT GCTGGAGTGG AGCACGATGA CGTAGCAGAG 1320  
 CTGCTGCAGG AGCTACAAAG CCTGGCCCAG TGCTACCAGG GTGGTGACAG CCTCGTGGAC 1380  
 TAAAGTTCCC AGTGTGGGAG AAAGGAGCTA GTTTGCAATA AAAACAGCTG GATGCAGGAG 1440  
 CCCAGTGTCT TCATGCAGAG GAGCTCAATG TCGCGGGACT AGCTACACCA ACATATGCAC 1500  
 TTTTACATT TAGAAACAT GTGATTAGAC CACAGAACAA TAAATATGTG CCATCAGACC 1560  
 AAAAAAAGT AGAGAAAGGA GCTGAATCC ACTCTCGATG CTATTTACAG AGGACATCTG 1620  
 TAAAGTCTTC ATAAAAGACC TTGAATGATG CCTAGGATGG CAGAGCCCCCT GGGTCCTACT 1680  
 CCATCCTCCA GCCTTTGTCC TTGTCTGGC CTCCTGCTCT CCAGATCTGT AAAGTGGGCT 1740  
 CAAGGACTGT ACAAGCAGAG TACAACCTACC CCCTCCCCGG TGCCAGGGCG CCTGTTGGGT 1800  
 TTGGTCCTGT GTAGATGATT CCCAGAGTCT CATTATCCA GCTCCTCTTC AGACAGAAGG 1860  
 TCCCCATGGT CAGACAGCTG GTCTGCATTG CTGGTACTGG TTGCATCATC CTCATCCTCA 1920  
 GAGCTGGCTT CACAGGCAGT GTGGAAGAGC TGCATGAGTT CTCGAAAACG GTGGGAAACC 1980  
 TCAGCAGGGG TCTTATTTCC CAGCTGCTGG GAGATGATGT TGAAGGTCTG TGGCTGTGCC 2040  
 CCTTGCTCCT GGCACATGGT GAGGATCACA CGGTACAGCT CCCTTGTTCA CAGGACAACC 2100  
 TTTTCCCCAG TGGAGCTGAC CTTGCTGTTG TTGGCACACA CCGTAGCTTC TGCGGCCTTT 2160  
 GGCTGCTGCT CCCCCTCTGG ACCCTTGCC TGTGTTCCAC TGTCTTTAGC CAAACCCCTT 2220  
 CTAGGGGCTT TGGGAGAAGT CTCTGAGGTG TCAATTCCTG ATGGAGATTC ATGGACAGGG 2280  
 CACGTCTGT CTCTTGTCTT CACCCTAGCT CTGCTTGAGG GCAGCCATCT CTCTTGAGTG 2340  
 TCTGGTTTCC CGGACACATG TCTTCTCCCT GCATCTCTGG TCTTTGAGGA AACAGGACTC 2400  
 AGGAAGGAAG CAGGGGGTTC CACGGTACCA GGCAATTTCT CAGTTTCTGA TGCATCCCAG 2460  
 ACCAGCATCA AAGCCTCTGA CTCACCTACT GCCTTTTGGC CCTCCCTCTC TTTCTGAAGT 2520  
 CTGGGGGATG CCTTGGGGCA GGAGCGAACC TCAGGCCCAA CCTGGTTTCT CTTAACAGTG 2580  
 TACAGTACAG CTCCAGTTGT GGGGGGAAAT TGAGGAGTCT CTGGTGAATG AGGTGGTGGG 2640  
 CCATCCAGGA GGAGCCGTTC TGTA 2664

09673395 "122700

## (2) INFORMATION ON SEQ ID NO. 538:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3888 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395 "122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

GAATTCCTCGC CCGGACTGAC GGAGCCCACT GCGGTGCGGG CGTTGGCGCG GGCACGGAGG 60  
 ACCCGGGCAG GCAGCGCAAG CGACCCCGAG CGGAGCCCCG GAGCCATGGC CCTGAGCGAG 120  
 CTGGCGCTGG TCCGCTGGCT GCAGGAGAGC CGCCGCTCGC GGAAGCTCAT CCTGTTTCATC 180  
 GTGTTCTCTG CGCTGCTGCT GGACAACATG CTGCTCACTG TCGTGGTCCC CATCATCCCA 240  
 AGTTATCTGT ACAGCATTAA GCATGAGAAG AATGCTACAG AAATCCAGAC GGCCAGGCCA 300  
 GTGCACACTG CCTCCATCTC AGACAGCTTC CAGAGCATCT TCTCCTATTA TGATAACTCG 360  
 ACTATGGTCA CCGGGAATGC TACCAGAGAC CTGACACTTC ATCAGACCGC CACACAGCAC 420  
 ATGGTGACCA ACGCGTCCGC TGTTCCTTCC GACTGTCCCA GTGAAGACAA AGACCTCCTG 480  
 AATGAAAACG TGCAAGTTGG TCTGTTGTTT GCCTCGAAAG CCACCGTCCA GCTCATCACC 540  
 AACCCTTTCA TAGGACTACT GACCAACAGA ATTGGCTATC CAATTCCCAT ATTTGCGGGA 600  
 TTCTGCATCA TGTTTGTCTC AACAAATTATG TTTGCCTTCT CCAGCAGCTA TGCCTTCCTG 660  
 CTGATTGCCA GGTGCTGCA GGGCATCGGC TCGTCTGCT CCTCTGTGGC TGGGATGGGC 720  
 ATGCTTGCCA GTGTCTACAC AGATGATGAA GAGAGAGGCA ACGTCATGGG AATCGCCTTG 780  
 GGAGGCCTGG CCATGGGGGT CTTAGTGGGC CCCCCCTTCG GGAGTGTGCT CTATGAGTTT 840  
 GTGGGGAAGA CGGCTCCGTT CCTGGTGCTG GCCGCCCTGG TACTCTTGA TGAGCTATT 900  
 CAGCTCTTTG TGCTCCAGCC GTCCCGGGTG CAGCCAGAGA GTCAGAAGGG GACACCCCTA 960  
 ACCACGCTGC TGAAGGACCC GTACATCCTC ATTGCTGCAG GCTCCATCTC CTTTGCAAAC1020  
 ATGGGCATCG CCATGCTGGA GCCAGCCCTG CCCATCTGGA TGATGGAGAC CATGTGTTCC1080  
 CGAAAGTGGC AGCTGGGCGT TGCCTTCTTG CCAGCTAGTA TCTCTTATCT CATTGGAACC1140  
 AATATTTTTG GGATACTTGC ACACAAAATG GGGAGGTGGC TTTGTGCTCT TCTGGGAATG1200  
 ATAATTGTTG GAGTCAGCAT TTTATGTATT CCATTTCCAA AAAACATTTA TGGACTCATA1260  
 GCTCCGAAC TTGGAGTTGG TTTTGCAAAT GGAATGGTGG ATTTCGTCAT GATGCCTATC1320  
 ATGGGCTACC TCGTAGACCT GCGGCACGTG TCCGTCTATG GGAGTGTGTA CGCCATTGCG1380  
 GATGTGGCAT TTTGTATGGG GTATGCTATA GGTCCTTCTG CTGGTGGTGC TATTGCAAAG1440  
 GCAATTGGAT TTCCATGGCT CATGACAATT ATTGGGATAA TTGATATTCT TTTTGCCCT1500  
 CTCTGCTTTT TTCTTCGAAG TCCACCTGCC AAAGAAGAAA AAATGGCTAT TCTCATGGAT1560  
 CACAACCTGCC CTATTAATAAC AAAAAATGAC ACTCAGAATA ATATCCAGTC ATATCCGATA1620  
 GGTGAAGATG AAGAACTCTGA AAGTGAAGTA GATGAGATCC TCAAAAATCA TCAAAGTGT1680  
 TAATTGTATA AAACAGTGTT TCCAGTGACA CAACTCATCC AGAACTGTCT TAGTCATACC1740  
 ATCCATCCCT GGTGAAAGAG TAAAACCAA GGTTATTATT TCCTTTCCAT GGTTATGGTC1800  
 GATTGCCAAC AGCCTTATAA AGAAAAAGAA GCTTTTCTAG GGGTTTGTAT AAATAGTGT1860  
 GAAACTTTAT TTTATGTATT TCATTTTATT AAATATCATA CAATATATTT TGATGAAATA1920  
 GGTATTGTGT AAATCTATAA ATACTTGAAT CCAAACCAA TATAATTTTT TAACCTACAT1980  
 TAACAAACAT TTGGGCAAAA ATCATATTGG TAATGAGTGT TTAAATTTAA AGCACACATT2040  
 ATCTCTGAGA CTCTTCCAAC AAAGAGAAAC TAGAATGAAG TCTGAAAAAC AGAATCAAGT2100  
 AAGACAGCAT GTTATATAGT GACACTGAAT GTTATTTAAC TTGTAGTTAC TATCAATATA2160  
 TTTATGCGTT AAACAGCTAG TTCTCTCAAG TGTAAGAGGAC AAGAACTGTG GTCAGTTATC2220  
 TTTTGAATCC ATAAATCTTA GCTGGCATTG GTTTTCTATG TAATCACCTA CCTAGAGAGA2280  
 GTTGTAATT ATATGTTAAC ATGTTATCTG GTTGGCAGCA AACACTAAAG CCAATAAAGG2340  
 AAAAAACAGTA AATGTTCCGA AAGCAGAGAA AAGCAACCAA ACATATTGTT ATGAACTAAA2400  
 AGCTTTCCCT TTAAGATGCA TACTTGTCTT ACTGGATGAA GAAAATTGAG GGTACATGTA2460  
 CCTTATACTG TCAAGGTTGT TTAAACATGA TAAGGTTAAT CGCCATCTAC TTCAAGTTT2520  
 AGAAAAGGAA ACAAGAAGCT AAAAACAGCT GCTCTGACTT TAATATCTGA CTATATCTTT2580  
 GATCTGTTTG CAGGTATCC AAGTGTTTT TAGGAATATA TTTATTTTAG GTTGTCTGAA2640  
 ACTACTATTT TTTAGACTCC TGAAAGTTGT TCACATCAAT GTGAAGACAA ATTTTAAATG2700  
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 CAGTGTGGAA TGTCTCTAAT ACTACTTGAG AATCCTGCAG TTCTATAATC ATAAACAAAA3000  
 ATTACTTAGT TTCGTTAAGC TAAGATTGTG TTTGTGTTAA CTTTCGACATC AAGGAGCAA3060  
 GAACTTTAGA ACAGACTCCT CAATCTTGTG ACTTTCTTAT TCTCTAGGAA AGTAACACTT3120  
 CGTTTCATGA AGCTTTTCTG TGGGGCTTCG ATTATTTCAA GTCTGGTTTC TAAGTGCAGT3180  
 GTGTTTGAAG CAAACGAACT TCCAACCTAC TTATTTGGCA TTGGGCAACT TGGCCAAGTC3240  
 TGCTACTTTG GAAGATGGCT CTGGAGGAAA CTCTCATATG GCTAAAAAGG CAGGCTAGTT3300  
 TCTTACTTCT ACAGGGGTAG AGCCTTAAAA AAGAACGTGC TACAAATTGG TTCTCTTTGA3360  
 GGGTTTCTGG TTCTCCCTGC CCCAATACC ATATACTTTA TTGCAATTTT ATTTTGCCT3420  
 TTACGGCTCT GTGTCTTTCT GCAAGAAGGC CTGGCAAAGG TATGCCTGCT GTTGGTCCCT3480  
 CGGGATAAGA TAAAATATAA ATAAAACCTT CAGAACTGTT TTGGAGCAAA AGATAGCTTG3540

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TACTTGGGGA AAAAAATTCT AAGTTCTTTT ATATGACTAA TATTCTTGGT TAGCAAGACT3600  
GGAAAGAGGT GTTTTTTTTAA AATGTACATA CCAGAACAAA GAACATACAG CTCTCTGAAC3660  
ATTTATTTTT TGAACAGAGG TGGTTTTTAT GTTTGGACCT GGTAATACAG ATACAAAAAC3720  
TTTAATGAGG TAGCAATGAA TATTCAACTG TTTGACTGCT AAGTGTATCT GTCCATATTT3780  
TAGCAAGTTT ACTTAATAAA TCTTCTGAAC CATGTTTTGT GCCTGTTTGT ATTCCTTTAT3840  
AAACCAAATG TTGTTGGAAT AAAATACATA AGGTATCATT TTGACCGT 3888

(2) INFORMATION ON SEQ ID NO. 539:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3304 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

AAACCCCTCTT GGCTGTCTGC TGTCCAGGGA GTCGCCACTC CCTTCATTAT AGCCTTGCTC 60  
 AGAGTGCAGC GGCAGGCCTG GGGATGGCCT CGGGAGAGGG ACCACAGAGC ACCAGCCTGC 120  
 ATGGAACCTC CTTCCTCACT CAGCTTCCCA CGTTGCCAGC TGGGACAGGG GAGATGGAGT 180  
 AATTTTGCTG TGGAAAGACT TCACGTCTTG CCGAATGAAA GTCCCGCCTG TCTGTCACGC 240  
 TGATGCCCCG GCAGCTGTCT GAGCACCCGG AATGGAATGA GTCTATGCAC TCCCTCCGGA 300  
 TCAGTGTGGG GGGCCTTCCT GTGCTGGCGT CCATGACCAA GGCCGCGGAC CCCCCTTCC 360  
 GCCCCCGCTG GAAGGTGATC CTGACGTTCT TTGTGGGTGC TGCCATCCTC TGGCTGCTCT 420  
 GCTCCCACCG CCCGGCCCCC GGCAGGCCCC CCACCCACAA TGCACACAAC TGGAGGCTCG 480  
 GCCAGGCGCC CGCCAACCTG TACAATGACA CCTACCCCTT GTCTCCCCCA CAAAGGACAC 540  
 CGGCTGGGAT TCGGTATCGA ATCGCAGTTA TCGCAGACCT GGACACAGAG CCAACCGCCC 600  
 AAGACGAAAA CACCTGGCGC AGCGACCTGA AAAAGGGCTA CCTGACCCTG TCAGACAGTG 660  
 GGGACAAGGT GGCCGTGGAA TGGGACAAAG ACCATGGGGT CCTGGAGTCC CACCTGGCGG 720  
 AGAAGGGGAG AGGCATGGAG CTATCCGACC TGATTGTTTT CAATGGGAAA CTCTACTCCG 780  
 TGGATGACCG GACGGGGGTC GTCTACCAGA TCGAAGGCAG CAAAGCCGTG CCCTGGGTGA 840  
 TTCTGTCCGA CGGCGACGGC ACCGTGGAGA AAGGCTTCAA GGCCGAATGG CTGGCAGTGA 900  
 AGGACGAGCG TCTGTACGTG GCGGCGCTGG GCAAGGAGTG GACGACCACT ACGGGTGATG 960  
 TGGTGAACGA GAACCCGGAG TGGGTGAAGG TGGTGGGCTA CAAGGGCAGC GTGGACCACG1020  
 AGAACTGGGT GTCCAACCTA AACGCCCTGC GGGCTGCTGC CGGCATCCAG CCGCCAGCTA1080  
 ACCTCATCCA TGAGTCTGCC TGCTGGAGTG ACACGCTGCA GCGCTGGTTC TTCCTGCCGC1140  
 GCCGCGCCAG CCAGGAGCGC TACAGCGAGA AGGACGACGA GCGCAAGGGC GCCAACCTGC1200  
 TGCTGAGCGC CTCCCCTGAC TTCGGCGACA TCGCTGTGAG CCACGTCGGG CGGGTGGTCC1260  
 CCACTCACGG CTTCTCGTCC TTCAAGTTCA TCCCCAACAC CGACGACCAG ATCATTGTGG1320  
 CCCTCAAATC CGAGGAGGAC AGCGGCAGAG TCGCCTCCTA CATCATGGCC TTCACGCTGG1380  
 ACGGGCGCTT CCTGTTGCCG GAGACCAAGA TCGGAAGCGT GAAATACGAA GGCATCGAGT1440  
 TCATTTAACT CAAAACGGAA AACTGAGCA AGGCCATCAG GACTCAGCTT TTATAAAAAC1500  
 AAGAGGAGTG CACTTTTGTT TTGTTTTGTT CTTTTTGAA CTGTGCCTGG GTTGGAGGTC1560  
 TGGACAGGGA GCCCAGTCCC GGGCCCCATA GTGGTGCGGG CACTGGACCC CCGGGCCCCA1620  
  
 CGGAGGCCGC GGTCTGAACT GCTTTCCATG CTGCCATCTG GTGGTGATTT CGGTCACTTC1680  
 AGGCATTGAC TCAAGGCCTG CCTAACTGGC TGGGTGCTTT CTTCCATCCG ACCTCGTTTT1740  
 TTTTCTTTCC TATGTTCTTT TGTTCACTGA ATATCCCTAG AGCTCCTACC ATATGTCAGG1800  
 CCCTATGCCT CACCCTGAGA ACGCAGTGAG CATGAGGTGG ACCTGTTTGC TGGGAACCCC1860  
 AGGTCACCCC CTTTTCTTCC CAAACTTGGT GCCTTGGAAG AATCAGGTCC AGCCCTGAAG1920  
 ATCCTTGGGG AAGAAAATGT TTATGTTGCA GGGTATTGCA TGGTCACGAG TGAGGGGCAG1980  
 GCCCCCTGGG GACACATCTG CCCACAGCTG CACAGGCCAG GGGCACAGGC ACATCTGTTG2040  
 GTTCTCAGGC CTCAGATAAA ACCATCTCCG CATCATATGG CCAGTGACCG CTTTCTCCCT2100  
 TCAAGAAAAA TCTGTGGCTG TGCAGTACTT TGAAGTTTTA ATTATTAACC CTGTTTAATT2160  
 AAAGCAGTTT CTTTTCTTAT AAAGTGGAAAT CACCAAATCT TATCACACAG AGCACAGTCC2220  
 TGTAATTACC CAGCCCCTC CAGCAGTGCG GGAGATTGTA AGGAAGCGGT GGCGGCTGGT2280  
 GAAGCAAGTC TCACATGTCT GCGTCTCTGG CCAATGGATA CAAAGATAAA GAAAATGTTG2340  
 CCTTTTTCTA GGAAGTGTCA GAAATCCTCA TGCCTTTCAA GACTTCTGTG AATGACTTGA2400  
 ATTTTTTATT CCCTGCCTAG GGTCTGTGAA CGAGGCCTGT CTCTTCCCTG GGGTTTCTTT2460  
 CCATGGCCTT TATTTCTCCT CTTCCAGTGG GAGTTTTGCA GGCTCTTCTC TGTGGAAACT2520  
 TCACGAGCGT TGGCTGGGCC TCGGCTTCGC TGGAGTGTA TCCAGGGTGA AGGCAGAGTG2580  
 GGATTTGAGA CCCAGGTTAG GCACGACCCA GGCTGAGAAG GGACGTTTCC ATCATTACA2640  
 GTGCCCTCCC CACAGCAACT ACCTCACCCC GACCCCCACC CTCCTCCTA CCCCACCCG2700  
 CGATCGTCAG GGGTGCCACG GTGGGCCGGA GGGTGCCGGC TCTGGCTGTC CCTGTGCCGG2760  
 TCCCTACAAA ACCTCTCCCC CTTTGAAACT CAAGCACAGC TCGGAGGAGG GCAGCGAGGA2820  
 GGGACCCCTC TCTCATGGTT GTCTCTTTCC CCCGCTATGT CATAGGTAGT GGAGGAAGCG2880  
 AAGGAAGTGA ACGCTGAATG TGACGCATTT CTGAAGAGCT CAGCTGTCAC CGGGCATAGC2940  
 CTGGAAGCCC CAAGTCTGTT CTGACTTTGC CTGGCTGTCT CCTTGACCCG CCTCCTAGAT3000  
 CATTGTCCTT GATGTCCAGG CTGGGTCAAT TAAAATAGAG ATGCAATCAG GAAGGTTGGG3060  
 GGAATTGGGA CTGTGGCTGA ATTGAGACCT TGCTGATGTA TTCATGTCAG CACCTGAGTC3120  
 ACAGCCCAGG TGCCCGGAAG CAGCCTCTTC GCATAGGCAG TGATTGCGA TTACTTTAAA3180  
 GCTCACCTTT TTTCTTCCCC TCTCTGTTCT CTGCTGTCAG CATAATGATT GTGTTCTTC3240  
 CCTATGGGAT CCATCTGTTT TGTAACAAT AAAGCGTCTG AGGGAGTGTA AAAACAGAT3300  
 GGAT

3304

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## (2) INFORMATION ON SEQ ID NO. 540:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 863 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

CAGGATTGAA ACAAGATGGC GGGTTCGTGG TGAGAAGCCG TCAAGGAGTA GAAATTGGTA 60  
 TGCTTAGAAG CAGATTCTAA AAGCAGTTTC TCTTCAGAAC ATCTTTTTTC ATACCACTTG120  
 ATAAGCATCT TGAAACACCA TGGCTGTAGC TGCAGTAAAA TGGGTGATGT CAAAGAGAAC180  
 TATCTTGAAA CATTTATTTT CAGTCCAAAA TGGAGCTTTA TATTGTGTTT GTCATAAATC240  
 TACGTATTCT CCTCTACCAG ATGACTATAA TTGCAACGTA GAGCTTGCTC TGACTTCTGA300  
 TGGCAGGACA ATAGTATGCT ACCACCCTTC TGTGGACATT CCATATGAAC ACACAAAACC360  
 TATCCCTCGG CCAGATCCTG TGCATAATAA TGAAGAAAACA CATGATCAAG TGCTGAAAAC420  
 CAGATTGGAA GAAAAAGTTG AACACCTTGA GGAAGGACCT ATGATAGAAC AACTTAGCAA480  
 AATGTTCTTT ACTACTAAGC ACCGTTGGTA TCCTCATGGA CGGTATCACA GATGTCGTAA540  
 GAATCTGAAT CCTCCAAAAG ACAGATGATG CGGAGGTTCC TGGGGGAATC AAAGAGAAAT600  
 GTGCCTCATT TGCCATTTGA GAAAATGCAG TCTGGTGTAT TCAGTAATAT ATAGTAAAGT660  
 AATAATGATA AAATATCTTT TCATATATTA GAATGTGTAC TTTTATATAA AGTAATTCTG720  
 GATTTGACAT TCTCATTTAG AGAGACCTAT TCCTTTTTTC GTTTTCTATT TTAGTGTTTC780  
 ATTTATGTGC GGTCTCCAAT TTAGGACTTT TCCATAGTGC CAAAGCCATA CATATTCAGT840  
 AGAACATCAA TAAAAAAAAA AAA 863

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## (2) INFORMATION ON SEQ ID NO. 541:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

ACCGACGGCC GCCCCTTTTC GTCTTTTTTT TTTTACATT TCAAATATAT TTTATTACTT 60  
TCCATCTTAG AAAGAATATG AAACCTGCAT GCAATGCTAA TGGTTTCTGA CATGTACATA 120  
GCATATAACA CAGCAGTACA ATGCGGCATA TACTGGGGGG CAGTGTGTGG AGGGGGCGTT 180  
CTTAAGGGTA TATGTACAGA GGAAAGGGCG CATGGTCATC TTAGCTTTCG AAAGAGGACT 240  
GCACTGTTTA ACATTGAAGA ATTACATGGG GAATCACAAA TATATTGCTT TAGTACTGCA 300  
TGTTCTGTTG TGGTGAGGGA AAGAAACATG CTTTGAAGGT TTTCCCTTGT CAACAGAATG 360  
TGTGTCTGTA GCTGTGTATT GCGCATGTAT TCATATATTT TTAAGTTTTC TCCTAAGGTT 420  
TTTGCTGACA GTGTTGGGAA CCTCACATGC TTCTGAAGCA TTAAATATTG AACCTGTGAA 480  
CCTTTCAGAA ATCCTCAGGT TGGGAAAGAC CCCACACCTT CTTTAAGGAT CATTGTGTCTC 540  
GCCATCACAG GATCTTGGA AATGTTTCTTA GGGTGTGTAA AAATTAACCA GGGGGGAATG 600  
AAGCACATTT TTCTGGCAAC CAACTTGAG TTCCTCAGAG AACAGATGCA GAGAGACCTG 660  
CTCCTGCTTG CCCGGCTACA GGGGCCACTG TGGAGTCACA CTGAGGCTGT GACCGGCCAT 720  
AAGCCCAGGA GAGCCCGTGG CAGCTGTGCC GAGGCGCCAG GACCTCTAAG CGGAAGCTTC 780  
CCAAGCTAGG AATGGAGCAA CACTGCAATG AAATGTGTCC ACCAAGCTCA TTGTTCTCTC 840  
CGGGCGCTTA TAAAGCTCAG ATGTATAGTG ACGTATGGAC AAATACAAAA AAAAAAAAAA 900  
AAAAAAAAAA AAAAAAGCC TTTCTTTCTC ACAGGCATAA GACACAAATT ATATATTGTT 960  
ATGAAGCACT TTTTACCAAC GGTCAGTTTT TACATTTTAT AGCTGCGTGC GAAAGGCTTC1020  
CAGATGGGAG ACCCATCTCT CTTGTGCTCC AGACTTCATC ACAGGCTGCT TTTTATCAAA1080  
AAGGGGAAAA CTCATGCCTT TCCTTTTTTA AAAATGCTTT TTTGTATTTG TCCATACGTC1140  
ACTATACATC TGAGCTTTAT AAGCGCCCGG GAGGAACAAT GAGCTTGGTG GACACATTTTC1200  
ATTGCAGTGT TGCTCCATTC CTAGCTTGGG AAGCTTCCGC TTAGAGGTCC TGGCGCCTCG1260  
GCACAGCTGC CACGGGCTCT CCTGGGCTTA TGGCCGGTCA CAGCCTCAGT GTGACTCCAC1320  
AGTGGCCCCCT GTAGCCGGGC AAGCAGGAGC AGGTCTCTCT GCATCTGTTT TCTGAGGAAC1380  
TCAAGTTTGG TTGCCAGAAA AATGTGCTTC ATTCCCCCTT GGTTAATTTT TACACACCCT1440  
AGGAAACATT TCCAAGATCC TGTGATGGCG AGACAAATGA TCCTTAAAGA AGGTGTGGGG1500  
TCTTTCCCAA CCTGAGGATT TCTGAAAGGT TCACAGGTTT AATATTTAAT GCTTCAGAAG1560  
CATGTGAGGT TCCCAACACT GTCAGCAAAA ACCTTAGGAG AAAACTTAAA AATATATGAA1620  
TACATGCGCA ATACACAGCT ACAGACACAC ATTCTGTTGA CAAGGGAAAA CCTTCAAAGC1680  
ATGTTTCTTT CCCTCACCAC AACAGAACAT GCAGTACTAA AGCAATATAT TTGTGATTCC1740  
CCATGTAATT CTTCAATGTT AAACAGTGCA GTCCTCTTTC GAAAGCTAAG ATGACCATGC1800  
GCCCTTTCCT CTGTACATAT ACCCTTAAGA ACGCCCCCTC CACACACTGC CCCCCAGTAG1860  
TACGCAGGCA TTGGTACCGG CTGGTGTAA AATGGCTATG GGACATGGTC AGGAAACCAT1920  
TTAGGCATTG GCATTGAGGG TTCCATAATC CGTTTCTAAG GA 1962

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## (2) INFORMATION ON SEQ ID NO. 542:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1772 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

```

TGGGGCGCTGT AGTCCGGCCG GAACCTGTTT GCGACCCCGA GTCCCATGAC ACCGCTTCTC 60
CTCACACCCC AGTCCGCAGT GCCCCTCCCC AGCCTCGGCC GGGCCTCCCG GGAGCCGGGC 120
GTGGCGTTCC AGCTAGTGAG CCGTTTCTCC CCTGGGCTCG GAGGCGGAAG CTTGAGGGGC 180
GCGGGGAGGA GCTTCGCGTG CGGGGTGAAC GCCCGCTCTA CGTGCTCGTT CTCTCGCGA 240
CCGCTGCGCG CGAGCCCCGT GTCCCCACGG CGGGCAGCAG CGCCGGCGGC GGCGGCTGAA 300
CGCGGAGGGG GCGGAGGGAG CCCGCGGCGG CGGCAGCAGC TACAGCGAAA TGGCGGAGAC 360
CGTGGCTGAC ACCCGGCGGC TGATCACCAA GCCGCAGAAC CTGAATGACG CCTACGGACC 420
CCCCAGCAAC TTCCTCGAGA TCGATGTGAG CAACCCGCAA ACGGTGGGGG TCGGCCGGGG 480
CCGCTTCACC ACTTACGAAA TCAGGGTCAA GACAAATCTT CCTATTTTCA AGCTGAAAGA 540
ATCTACTGTT AGAAGAAGAT ACAGTGACTT TGAATGGCTG CGAAGTGAAT TAGAAAGAGA 600
GAGCAAGGTC GTAGTTCCCC CGTCCCCTGG GAAAGCGTTT TTGCGTCAGT TCCTTTTAGA 660
GGAGATGATG GAATATTTGA TGACAATTTT ATTGAGGAAA GAAAACAAGG GCTGGAGCAG 720
TTTATAAACA AGGTCGCTGG TCATCCTCTG GCACAGAACG AACGTTGTCT TCACATGTTT 780
TTACAAGATG AAATAATAGA TAAAAGCTAT ACTCCATCTA AAATAAGACA TGCCTGAAAT 840
TTGGCAAGAA GGGGCAAAAA CGTGACTATT AATGATTGAT AAGCACCAGT GAAGAAGTTC 900
TAACTTTTAG CATGCTGCAC AGAAACTGGT ATAACATGCC TTCAGTATAC TAACACTCAT 960
ATGCTCAGTT TTGTTTGTGTT TTGGCAGTTG ACAAGAAGTT AATTTGCTTT AGTAAAAATC1020
CCTCATTCCA GCCTTCTAT ATAAATAGCT CTTTCTTGCT GTTTAATGT GGTGCACACT1080
ATAGCCTCAC AAACCTGTTA TTCCAGTGTA ATCTGCAGTG TCGTAACTAA AGTTACTGGC1140
TTGGTCTTAT TTGCACAGTT TTTGCGTCTT GTTTGCTTCT TGCATCTGAT TAACTAGAAT1200
ATTTCTCTTT CCCCCTTTTA ATTTGTGATG TCACTTGACC CCATTTATGT GTAGGAGCAC1260
TACACCATTG GTTTCCAATA CTGCACACAT AAGATACATA CTTGTGTGCA GAAAGTATCT1320

TCCTCCAGGC TTGTAATACC CTTACATGAG AAGATTAATG AGGGAAATCT TTATATTCTG1380
TATAAAAACA AAAGCAAATT TATATACTAA AATCATTTGT CTAAAAATTT AAGTTGTTTT1440
CAAATAAAAA TTAAATGCA TTTCTGATAT GCACTGATTG TGTTGCCTCC AGCTTTTTTT1500
GCTCTCTATG AGTGACTACT TAAGTCACTT GTTGAGAGGG ATTATTTACT AATTATATAC1560
TTCTCATTCC TGTAACCTCA TTCCCTTTAA ACAGTGGTGA TATCAAATAT ACTTCCATCC1620
ATTGAATGGG GTATTTTAA CAACAACAAA AGTGATATAC TAAAAAATGT ATTGCTTAAG1680
GCTTATTGAA TCATTTTGAA GCACTTTGTG TATTTGAAAA CTGCTTTATA ATCTCATTTA1740
TAAAAAGGAC TTTCAAAGAT AAAACCAAAA AA

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1772

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## (2) INFORMATION ON SEQ ID NO. 543:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1009 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

```

CTCGTGCGGT GATGTTGAGC AGAAGATACA ATTCAAAAGA GAAACAGCCA GTTTGAAACT 60
GTTACCCAC CAGCCCCGAA TTGTGGAGAT GAAGAAAGGA AGCAATGGCT ATGGTTTCTA 120
TCTGAGGGCA GGCTCAGAAC AGAAAGGTCA AATCATCAAG GACATAGATT CTGGAAGTCC 180
AGCAGAGGAG GCTGGCTTGA AGAACAATGA TCTGGTAGTT GCTGTCAACG GCGAGTCTGT 240
GGAAACCCTG GATCATGACA GTGTGGTAGA AATGATTAGA AAGGGTGGAG ATCAGACTTC 300
ACTGTTGGTG GTAGACAAAG AGACGGACAA CATGTACAGA CTGGCTCATT TTTCTCCATT 360
TCTCTACTAT CAAAGTCAAG AACTGCCCCA TGGCTCTGTC AAGGAGGCTC CAGCTCCTAC 420
TCCCATTCT CTGGAAGTCT CAAGTCCACC AGATACTACA GAGGAAGTAG ATCATAAGCC 480
TAAACTCTGC AGGCTGGCTA AAGGTGAAAA TGGCTATGGC TTTCCTTAA ATGCGATTCTG 540
GGGTCTGCCA GGCTCATTCA TCAAAGAGGT ACAGAAGGGC GGTCTGCTG ACTTGGCTGG 600
GCTAGAGGAT GAGGATGTCA TCATTGAAGT GAATGGGGTG AATGTGCTAG ATGAACCCTA 660
TGAGAAGGTG GTGGATAGAA TCCAGAGCAG TGGGAAGAAT GTCACACTTC TAGTCTGTGG 720
AAAGAAGGCC TATGATTATT TCCAAGCTAA GAAAATCCCT ATTGTTCCCT CCCTGGCTGA 780
TGCCAGTTGA CAGCCCTGCA GGTCTAAAG AAGGAATAGT GGTGGAGTCA AACCATGACT 840
CGCACATGGC AAAAGAACGG GCGGCTATTG CAGACGGCTA ATTTATGCTT AACTTAGGAA 900
GAGATAAGGT TCCTTGAGCA CCAAAGATGA TTCATAACTC TGTATAGGTG ACAGCTGCTT 960
ATAAAAGCAT CTTAGCAGAT AAGCCTATTA AAATTGTGCT TTTGTAACA 1009

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## (2) INFORMATION ON SEQ ID NO. 544:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2834 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00/221" 56EE/960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

CACTTTGCGG GCGGCACTTT TTCCAGGTTG TTAATCCAGC TAATGGAGAA GGATAGATGC 60  
 ACGCTACTTG GTTTAGAAAA AAAAACAAAA ATGAGCAAAC GAGACGCCCC TTCCGTTTTTA 120  
 TGATAACTAA GCTGCAGGGA AATAAATCGG CTGGCCCTAC TGCAATCTAC TGCACTCGAG 180  
 AAACATCACA GAAAATTCTT TGATTTATCT TAATAGTGAC AAGTGAGCCT GCTTCTGTCA 240  
 ATTACTGAAG CTATAAGGAG ATTTTTTAAA AATTAAACTT CAACACAATG AGGTGTTGCC 300  
 ACATCTGCAA ACTTCCTGGG AGAGTAATGG GGATTCGAGT GCTTCGATTA TCTTTGGTGG 360  
 TCATCCTCGT ATTATTACTG GTAGCTGGTG CTTTGACTGC CTTACTTCCC AGTGTTAAAG 420  
 AAGACAAGAT GCTCATGTTG CGTAGGGAAA TAAAATCCCA GGGCAAGTCC ACCATGGACT 480  
 CCTTTACTCT CATAATGCAG ACGTACAACA GAACAGATCT CTTATTGAAA CTTTTAAATC 540  
 ATTATCAGGC TGTACCAAAT CTGCACAAAG TGATTGTGGT ATGGAACAAT ATGGAGAGA 600  
 AGGCACCAGA TGAGTTATGG AATTCTCTAG GGCCCCACCC TATCCCTGTG ATCTTCAAAC 660  
 AACAGACAGC AAACAGGATG AGAAATCGAC TCCAGGTCTT TCCTGAACTG GAAACCAATG 720  
 CAGTGTTGAT GGTAGATGAT GACACACTCA TCAGCACCCC AGACCTTGTT TTTGCTTTCT 780  
 CAGTTTGGCA GCAATTTTCT GATCAAATTG TAGGATTTGT TCCTAGAAAAG CACGTCTCTA 840  
 CTTTCATCAGG TATCTACAGT TATGGAAGTT TTGAAATGCA AGCACCAGGG TCTGGAAATG 900  
 GTGACCAGTA CTCTATGGTG CTGATTGGAG CCTCATTCTT CAATAGCAAA TATCTTGAAT 960  
 TATTTTCAGAG GCAACCTGCA GCTGTCCATG CTTTGATAGA TGATACTCAA AACTGTGATG1020  
 ATATTGCCAT GAATTTTATC ATTGCCAAGC ATATTGGCAA GACTTCAGGG ATATTTGTGA1080  
 AGCCTGTAAA CATGGACAAT TTGGAAAAAG AAACCAACAG TGGCTATTCT GGAATGTGGC1140  
 ATCGAGCTGA GCACGCTCTG CAGAGGTCTT ATTGTATAAA TAAGCTTGTT AATATCTATG1200  
 ATAGCATGCC CTTAAGATAC TCCAACATTA TGATTTCCCA GTTTGGTTTT CCATATGCCA1260  
 ACTACAAAAG AAAAAATATA AAGTAAAACA AACCTGAAAA CTGCTTGGCA1320  
 TTTGAGTAGC TTCTCCATGC TATGTATTTT TTTAAGCAAC ATCATGAAT TTATCTACTC1380  
 CAGAAGTCTC TACAATAGAA AAAAAAGTGC AGTGCTTCTA GGATATAAAA TTCACATTAC1440  
 TTTTGAAAGC CAAGAAGTTG GTCTTATCCA GTTAGGTCTT CTTATGAAGA GTTTTCATCC1500  
 AGGGATATAA CTCCTTGGTC AGTGATTTTA TTGTTTACAT CCTGAGACTG TTCTACAGTT1560  
 TCTTTGACTC CTGGCATTG CCTTAAGGAC CTATAGCAAG CTGTTTCTAG GATCAGAAAC1620  
 TCAAGAGAGG CATTTCTCTG CTTTTTCACT AAAGGTCAGT TGTTTTAATT TGAAACCTGA1680  
 AATGCCTCTT TAGCAAAAGC CTGTGGTATG GGGTAAAGCC ATGTAAGAAG AGAATAGTCT1740  
 CAGTCACATA TGAAGAGGAA AATTTGCAGC TGCCAGTGCT TTCCTTGTTG CCCTGCCAAC1800  
 CAGCTCTTCC AGGACGAAC TGTCCAGCA TGTTTTTGAT GTAACCATCC ATGCTTTTAT1860  
 TTTTGTTAAG TCTTTTGTGA CTGGGACAGT TAATTTTAGT AGCTGAAGAA CGTCTAGTTG1920  
 TTTGCTTGAT ATTTGTGAAC ATTTACTGCA TGGATCACAA AACAATATAC CCTGTATTTT1980  
 TTACACGCCA CTTATATGCA GCAAGGAGTA AATGTGTTAC TAGATTCGGG TAGTGCATTT2040  
 TGTCACTGAA TCTGACCTTG AGAATGTACA TTAATTCTTA TATTTTACAT AATGTATGTG2100  
 TTGTTTTAAGA AATGTATAAA AAACCTGAAA AAAATGAGTA AGAACTGGCA GAAGTTAAAA2160  
 CCCTTTGTAT CAAAAGATCT TTATTGGTAG AGCACTGGTT ATCTTCTGGA TACTAAAAAG2220  
 TTGTATTACA AAGCCAAACA CTTGCATTCA CAACTTTAAA AAAAGATCCA AGGAACATT2280  
 CATAATGATG AAATTCCAAC TACATACAAG GAGGAGAAAA TAAGAACCCA GTCATAACAG2340  
 AGGAATTCTA TAGGAGTCTG CATCAATTCA TTCTTAAGGT TGCCTACTCT CTGTTATGTG2400  
  
 AATTAGCGTC TGTGTTTCAC CCATTGTCTG TGTTTAGTCC TTGTTTACCA CTAAGGCAAG2460  
 GAATTCTTAA CTAGGCCTCT GTTTACCAAC TTCTCTTTCT CCTCCTTTCC CTCTTATTCC2520  
 TCCTTCTCCT CTTCTTCTT ATATAATGCT AGTATATTCT CAAAATTGCA AAGCTGTGAG2580  
 AATATTAATA TAATCATGGC TAATGTTCCA ATAATGAGGT CTTTGTGCAT TTAGTTCGGC2640  
 ATATGATGGT TTTTTTTT CATTAAAGAG TATATGTGTC TTAATGCAGT CAGATTGTAA2700  
 AAAACAAAAA CAAAGAACT AAGAATCTTA CTAAAAATCG ATAATGTCAG TTATCTGTTT2760  
 TGTTCAATAT TGGTAGTACT TTTTGCCTC TTATGATTCC TCTAGCAGAT AAATAAAAGA2820  
 AACTTTTGCC ATCC 2834

0063395 122700

## (2) INFORMATION ON SEQ ID NO. 545:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2319 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

AACGTCATTG GTAACAGCAA GTCCCAGACA CCAGCCCCCA GTTCCGAAGT GGTTTTGGAT 60  
TCAAAGAGAC AAGTTGAGAG AGAGGAAACC AACCATGAGA TCCAGGAGGG GAAAGAAGAG 120  
CCTCAGAGGG ACAGGCTGCC GCAGGAGCCA GGCCGGGAGC AGGTNGTGGA AGACAGACCT 180  
GTAGGTGGAA GAGGCTTCGG GGGAGCCGGA GAATGGGGCC AGACCCACAC GGTGCAGGCT 240  
GCCCTGTCAG TGAGNCCAGG AAAATCCAGA GATGGAGGGC CCTGAGCGAG ACCAGCTTGT 300  
CATCCCCGAC GGACAGGAGG AGGAGCAGGA AGCTGCCGGG GAAGGGAGAA ACCAGCAGAA 360  
ACTGAGAGGA GAAGATGACT ACAACATGGA TGAAAATGAA GCAGAATCTG AGACAGACAA 420  
GCAAGCAGCC CTGGCAGGGA ATGACAGAAA CATAGATGTT TTTAATGTTG AAGATCAGAA 480  
AAGAGACACC ATAAATTTAC TTGATCAGCG TGAAAAGCGG AATCATACAC TCTGAATTGA 540  
ACTGGAATCA CATATTTTCA AACAGGGCCG AAGAGATGAC TATAAAATGT TCATGAGGGA 600  
CTGAATACTG AAAACTGTGA AATGTACTAA ATAAATGTGA CATCTGAANG ATGATTATTG 660  
TGNAAAATTT AGTATGCACT TTGTGTAGGA AAAAATGGNA ATNGGTCTTT TAAACAGCTT 720  
TTGGGGGGNT ACTTTNGGAA GTGTCTNAAT AANGGTGTCA CNAATTTTGT GNTAGTANGG 780  
TATTTCTGTA GNAAGNNTTC AACACCAAAA CTNGGAACAT AGTTCTCCTT CAAGTGTGG 840  
CGACANCGGG NNGCTTCCTG ATTCTGGAAT ATAACCTTGT GTAAATTAAC AGCCACCTAT 900  
AGAAGAGTCC ATCTGCTGTG AAGGAGAGAC AGAGAACTCT GGGTTCCGTC GTCCTGTCCA 960  
CGTGCTGTAC CAAGTGCTGG TGCCAGCCTG TTACCTGTTT TCACTGAAAA GTCTGGCTAA1020  
TGCTCTTGTT TAGTCACTTC TGATTCTGAC AATCAATCAA TCAATGGNCC TAGANGCACT1080  
GACTGTTAAC ACAAACGTCA CTAGNCAAAG TAGNCAACNA GCTTTAAGTC TAAATACAAA1140  
GCTGTTCTGT GTGAGAATTT TTTAAAAGGC TACTTGTATA ATAACCCTTG TCATTTTAA1200  
TGTACAAAAC GCTATTAAGT GGCTTAGAAT TTGAACATTT GTGNTCTTT ATTTACTTTG1260  
CTTNCGTGTG TGGGCAAAGC AACATCTTCC CTAATATAT ATTACCAAGA AAANGCAAGA1320  
AGCAGATTAG GNTTTTTGAC NNAAAACANA ACAGGCCNNA AAAGGGGGCN TGNACCTGGA1380  
GCAGAGCATG GTGNAGAGGC AAGGCATGNA GAGGGCAAGT TTGTTGTGGA CAGATCTGTG1440  
CCTACTTTAT TACTGGAGTA AAANGAAAAC AAAGTTNCAT TGATGTCGNA AGGATATATA1500  
  
CAGTGTTNAG AAATTNNAGG NACTNGTTN AGAAAAACAG GAATACNNA TGGNTTGNNT1560  
TTTATCATAN GTGNTACACA TTTAGCTTGT GGNTAAATNG ACTCACAAA CTGANTTTTA1620  
AAATCAAGTT AATGTGAATT TTGAAAATTA CTACTTAATC CTAATTCACA ATAACAATGG1680  
CATTAAGGTT TGACTTGAGT TGGTTCTTAG TATTATTTAT GGTAAATAGG CTCTTACCAC1740  
TTGCNAAATA ACTGGNCCAC ATCATTAATG ACTGACTTCC CNAGTAANGG CTCTCTAAGG1800  
GGTAAGTNAG GAGGATCCAC AGGATTTGAG ATGCTAAGGC CCCAGAGATC GTTTGATNCC1860  
AACCCTCTTA TTTTCNAGAG GGGAAAATGG GGCTNAGNA AGTTACANGA GCATCNTNAG1920  
CNTGGTGCGC TGGNCACCCC NTGGCCNTG ACACNAGACT CCCNGAGTAG CTGGGANCTA1980  
CAGGCACACA GTCATGAAG CAGGCCNTG TTTGCAATTC ACGTTGCCNA CCTNCCAACN2040  
TTAAACATTN CTTCATATGT GATGTCCTTA GTCACNTAAG GTTAAANCTT TNCCACCCA2100  
GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC TCTTCTAANG TCCTCTTCCA2160  
GCCTCACTTT GAGTCCTCCT TNGGGGTTGA TNNNAGGAAT TTTCTCTTGC TTTCTCAATA2220  
AAGTCTCTAT TCATCTCATG TTTAATTTGT ACGCATAGAA TTGCTGAGAA ATAAATGTT2280  
CTGTTCAACT TANNNNNAAA AAAAAAANA AAAAAAAA 2319

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 546:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2456 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| TGCAACTGTG | CACCCAGCTT | GCCAGATTTT | TCCCCATTAC | ACCCCCAGTG  | TGGCATATCC | 60   |
| TTGGTCCCCA | GAGGCACACC | CCTTGATCTG | TGGACCTCCA | GGCCTGGACA  | AGAGGCTGCT | 120  |
| ACCAGAAACC | CCAGGCCCTT | GTTACTCAA  | TTCACAGCCA | GTGTGGTTGT  | GCCTGACTCC | 180  |
| TCGCCAGCCC | CTGGAACCAC | ATCCACCTGG | GGAGGGGCTT | TCTGAATGGA  | GTTCTGACAC | 240  |
| CGCAGAGGGC | AGGCCATGCC | CTTATCCGCA | CTGCCAGGTG | CTGTCGGCCC  | AGCCTGGCTC | 300  |
| AGAGGAGGAA | CTCGAGGAGC | TGTGTGAACA | GGCTGTGTGA | GATGTTTCAGG | CCTAGCTCCA | 360  |
| ACCAAGAGTG | TGCTCCAGAT | GTGTTGGGGC | CCTAACTTGG | CACAGAGTCC  | TGCTCCTGGG | 420  |
| AAAGGAAAGG | ACCACAGCAA | ACACCATTCT | TTTTGCCGTA | CTTCCTAGAA  | GCACTGGAAG | 480  |
| AGGACTGGTG | ATGGTGGGAG | GGTGAGAGGG | TGCCGTTTTT | CTGCTCCAGC  | TCCAGACCTT | 540  |
| GTCTGCAGAA | AACATCTGCA | GTGCAGCAAA | TCCATGTCCA | GCCAGGCAAC  | CAGCTGCTGC | 600  |
| CTGTGGCGTG | TGTGGGCTGG | ATCCCTTGAA | GGCTGAGTTT | TTGAGGGCAG  | AAAGCTAGCT | 660  |
| ATGGGTAGCC | AGGTGTTACA | AAGGTGCTGC | TCCTTCTCCA | ACCCCTACTT  | GGTTTCCCTC | 720  |
| ACCCCAAGCC | TCATGTTTAT | ACCAGCCAGT | GGGTTCAGCA | GAACGCATGA  | CACCTTATCA | 780  |
| CCTCCCTCCT | TGGGTGAGCT | CTGAACACCA | CGTTTGGCCC | CTCCACAGTA  | AGGCTAGTAC | 840  |
| ATTGAGGGGC | AACCCTGGGC | TCTATCATTT | TCCTTTTTTG | CCAAAAGGAC  | CAGTAGCATA | 900  |
| GGTGAGCCCT | GAGCACTAAA | AGGAGGGGTC | CCTGAAGCTT | TCCCACTATA  | GTGTGGAGTT | 960  |
| CTGTCCCTGA | GGTGGGTACA | GCAGCCTTGG | TTCCTCTGGG | GGTTGAGAAT  | AAGAATAGTG | 1020 |
| GGGAGGGAAA | AACTCCTCCT | TGAAGATTTT | CTGTCTCAGA | GTCCCAGAGA  | GGTAGAAAGG | 1080 |
| AGGAATTTCT | GCTGGACTTC | ATCTGGGCAG | AGGAAGGATG | GAATGAAGGT  | AGAAAAGGCA | 1140 |
| GAATTACAGC | TGAGCGGGGA | CAACAAAGAG | TTCTTCTCTG | GGAAAAGTTT  | TGTCTTAGAG | 1200 |
| CAAGGATGGA | AAATGGGGAC | AACAAAGGAA | AAGCAAAGTG | TGACCCTTGG  | GTTTGGACAG | 1260 |
| CCCAGAGGCC | CAGCTCCCCA | GTATAAGCCA | TACAGGCCAG | GGACCCACAG  | GAGAGTGGAT | 1320 |
| TAGAGCACAA | GTCTGGCCTC | ACTGAGTGGA | CAAGAGCTGA | TGGGCCTCAT  | CAGGGTGACA | 1380 |
| TTCACCCACG | GGCAGCCTGA | CCACTCTTGG | CCCTTCAGGC | ATTATCCCAT  | TTGGAATGTG | 1440 |
| AATGTGGTGG | CAAAGTGGGC | AGAGGACCCC | ACCTGGGAAC | CTTTTTCCCT  | CAGTTAGTGG | 1500 |
| GGAGACTAGC | ACCTAGGTAC | CCACATGGGT | ATTTATATCT | GAACCAGACA  | GACGCTTGAA | 1560 |
| TCAGGCACTA | TGTTAAGAAA | TATATTTATT | TGCTAATATA | TTTATCCACA  | AATGTGGTCT | 1620 |
| GGTCTTGTGG | TTTTGTTCTG | TCGTGACTGT | CACTCAGGGT | AACAACGTCA  | TCTCTTTCTA | 1680 |
| CATCAAGAGA | AGTAAATTAT | TTATGTTATC | AGAGGCTAGG | CTCCGATTCA  | TGAAAGGATA | 1740 |
| GGGTAGAGTA | GAGGGCTTGG | CAATAAGAAC | TGGTTTGTA  | GCCCCATAAA  | GTGTGGCTTA | 1800 |
| GTGAGATGCA | GGAAGGAGAA | AGCATGACTG | GATTCTTACT | GTGCTTCAGT  | CATTATTATT | 1860 |
| ATATGTTTCA | CTTCACACAT | TATCATACTT | CAGTGACTCA | GACCTTGGGC  | AAATACTCTG | 1920 |
| TGCCTCGCTT | TTTCAGTCCA | TAAAATGGGC | CTACTTAATA | GTTGTTGCAG  | GACTTACATG | 1980 |
| AGATAATAGA | GTGTAGAAAA | TATGTTCCAA | AGTGGAAGT  | TTTATTTCAGT | GATGAAAAAC | 2040 |
| ATCCAAACCT | GTCACAGAGC | CCATCTGAAC | ACAGCATGGG | ACCGCCAACA  | AGAAGAAAAG | 2100 |
| CCGCCCCGAA | GCAGCTCAAT | CAGGAGGCTG | GGCTGGAATG | ACAGCGCAGC  | GGGGCCTGAA | 2160 |
| ACTATTTATA | TCCCAAAGCT | CCTCTCAGAT | AAACACAAAT | GACTGCGTTC  | TGCCTGCACT | 2220 |
| CGGGCTATTG | CGAGGACAGA | GAGCTGGTGC | TCCATTGGCG | TGAAGTCTCC  | AGGGCCAGAA | 2280 |
| GGGGCCTTTG | TCGCTTCCTC | ACAAGGCACA | AGTTCCTTCT | CTGCTTCCCC  | GAGAAAAGGT | 2340 |
| TGGTAGGGGT | GGTGGTTTAG | TGCCTATAGA | ACAAGGCATT | TCGCTTCCTA  | GACGGTGAAA | 2400 |
| TGAAAGGGAA | AAAAAGGACA | CCTAATCTCC | TACAAATGGT | CTTTAGTAAA  | GGAACC     | 2456 |

096335 12700

## (2) INFORMATION ON SEQ ID NO. 547:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2218 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

GAGGAAAAAG AACAAATGAAC AGCAACGATC TTGACTGTGC AACTCAGACA TTCCTGCAGA 60  
AAAGACATAT GTTGCTTTAC AAGAAGGCCA AAGAAGCTATG GGGCCTTCCC AGCATTGAC 120  
TGTTTCATTGC ATAGAATGAA TTAAATATCC AGTTACTTGA ATGGGTATAA CGCATGAATG 180  
TGTGATTTTA TTAGGGGCAT CTGCCAATTC TCTCACTGTG GTTCCTTCTC TGACTTTGCC 240  
TGTTTCATCAT CTAAGGAGGC TAGATCCTTC GCTGACTTCA CCATTCCTCA AACCTGTAAG 300  
TTTCTCACTT CTTCCAAATT GGCTTTGGCT CTTTCTTCAA CCTTTCCATT CAAGAGCAAT 360  
CTTTGCTAAG GAGTAAGTA ATGTGAAGAG TACCAACTAC AACAAATCTA CAGATAATTA 420  
GTGGATTGTG TTGTTTGTG AGAGTGAAGG TTTCTTGGCA TCTGGTGCCT GATTAAGGCT 480  
TGAGTATTAA GTTCTCAGCA TATCTCTCTA TTGTCTTGAC TTGAGTTTGC TGCATTTTCT 540  
ATGTGCTGTT CGTGACTTGG AGAACTTAAA GTAATCGAGC TATGCCAACT TGGGGTGGTA 600  
ACAGAGTACT TCCCACCACA GTGTTGAAAG GGAGAGCAAA GTCTTATGGA TAAACCCTCC 660  
TTTCTTTTGG GGACACATGG CTCTCACTTG AGAAGCTCAC CTGTGCTGAA TGTCCACATG 720  
GTCATAAAC ATGTTATCCT TAAACCCCC GTATGCCTGA GTTGAAAGGG CTCTCTCTTA 780  
TTAGGTTTTT ATGGGAACAT GAGGCAGCAA ATCTATTGCT AAGACTTTAC CAGGCTCAAA 840  
TCATCTGAGG CTGATAGATA TTTGACTTGG TAAGACTTAA GTAAGGCTCT GGCTCCCAGG 900  
GGCATAAGCA ACAGTTTCTT GAATGTGCCA TCTGAGAAGG GAGACCCAGG TTATGAGTTT 960  
TCCTTTGAAC ACATTGGTCT TTTCTCAAAG TTCCTGCCTT GCTAGACTGT TAGCTCTTTG 1020  
AGGACAGGGA CTATGTCTTA TCAATCACTA TTATTTTCCT GTTACCTAGC ATGGGACAAG 1080  
TACACAACAC ATATTGTGT AGTCTTCTAA AAGACTCCTC TGATTGGGAG ACCATATCTA 1140  
TAATTGGGAT GTGAATCATT TCTTCAGTGG AATAAGAGCA CAACGGCACA ACCTTCAAGG 1200  
ACATATTATC TACTATGAAC ATTTTACTGT GAGACTCTTT ATTTTGCCTT CTACTTGC 1260  
TGAAATGAAA CCAAAACAGG CCGTTGGGTT CCACAAGTCA ATATATGTTG GATGAGGATT 1320  
CTGTTGCCTT ATTGGGAACT GTGAGACTTA TCTGGTATGA GAAGCCAGTA ATAAACCTTT 1380  
GACCTGTTTT AACCAATGAA GATTATGAAT ATGTTAATAT GATGTAAATT GCTATTTAAG 1440  
TGTAAGCAG TTCTAAGTTT TAGTATTTGG GGGATTGGTT TTTATTATTT TTTTCCTTTT 1500  
TGAAAAATAC TGAGGGATCT TTTGATAAAG TTAGTAATGC ATGTTAGATT TTAGTTTTCG 1560  
AAGCATGTTG TTTTCAAAT ATATCAAGTA TAGAAAAAGG TAAAACAGTT AAGAAGGAAG 1620  
GCAATTATAT TATTTCTCTG TAGTTAAGCA AACTTTGTT GAGTGCCTGC TATGTGCACG 1680  
GCATGGGCCC ATATGTGTGA GGAGCTTGTC TAATTATGTA GGAAGCAATA GATCTCGGTA 1740  
GTTACGTATT GGGCAGATAC TTAGTGTATG AATGAAAGAA CATCACAGTA ATCACAATAT 1800  
CAGAGCTGAG TTATCCCCAG TGTAGCTTCG TTGGGGATTG CAGTTTCTGG GAACGAGAGT 1860  
TAGGGCCATT TTATTTAAAA GAAACTCCCG GTTGAGACCG GTTCTTATGA ACCTCTGAAA 1920  
CGTACAAGCC TTCACAAGTT TAACTAAATT GGGATTAATC TTTCTGTAGT TATCTGCATA 1980  
ATTCTTGTTT TTCTTTCCAT CTGGCTCCTG GGTTGACAAT TTGTGGAAAC AACTCTATTG 2040  
CTACTATTTA AAAAAATCA GAAATCTTTC CCTTTAAGCT ATGTTAAATT CAACTATTTC 2100  
CTGCTATTCC TGTTTTGTCA AAGAATTATA TTTTCAAAA TATGTTTATT TGTTGATGGT 2160  
GTCCCAGGAA AACTAATAA AAACCACAGA GACCAGCCCC AAAAAAAAAA AAGTTTTG 2218

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## (2) INFORMATION ON SEQ ID NO. 548:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2196 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| CGGCGCGATG  | CGCGGAGACC | CCCGCGGGGG | CGGCGGCGGC | CGTGAGCCCC | GATGAGGCCC | 60   |
| GAGCGTCCCC  | GGCCGCGCGG | CAGCGCCCCC | GGCCCGATGG | AGACCCCGCC | GTGGGACCCA | 120  |
| GCCCGCAACG  | ACTCGCTGCC | GCCACGCTG  | ACCCCGGCCG | TGCCCCCTA  | CGTGAAGCTT | 180  |
| GGCCTCACCG  | TCGTCTACAC | CGTGTCTAC  | GCGCTGCTCT | TCGTGTTTCT | CTACGTGCAG | 240  |
| CTCTGGCTGG  | TGCTGCGTTA | CCGCCACAAG | CGGCTCAGCT | ACCAGAGCGT | CTTCCTCTTT | 300  |
| CTCTGCCTCT  | TCTGGGCCTC | CCTGCGGACC | GTCCTCTTCT | CCTTCTACTT | CAAAGACTTC | 360  |
| GTGGCGGCCA  | ATTCGCTCAG | CCCCTTCGTC | TTCTGGCTGC | TCTACTGCTT | CCCTGTGTGC | 420  |
|             |            |            |            |            |            |      |
| CTGCAGTTTT  | TCACCCTCAC | GCTGATGAAC | TTGTACTTCA | CGCAGGTGAT | TTTCAAAGCC | 480  |
| AAGTCAAAAT  | ATTCTCCAGA | ATTACTCAA  | TACCGGTTGC | CCCTCTACCT | GGCCTCCCTC | 540  |
| TTCATCAGCC  | TTGTTTTCT  | GTTGGTGAAT | TTAACCCTGT | CTGTGCTGGT | AAAGACGGGA | 600  |
| AATTGGGAGA  | GGAAGGTTAT | CGTCTCTGTG | CGAGTGGCCA | TTAATGACAC | GCTCTCTGTG | 660  |
| CTGTGTGCCG  | TCTCTCTCTC | CATCTGTCTC | TACAAAATCT | CTAAGATGTC | CTTAGCCAAC | 720  |
| ATTTACTTGG  | AGTCCAAGGG | CTCCTCCGTG | TGTCAAGTGA | CTGCCATCGG | TGTCACCGTG | 780  |
| ATACTGCTTT  | ACACCTCTCG | GGCCTGCTAC | AACCTGTTCA | TCCTGTCAAT | TTCTCAGAAC | 840  |
| AAGAGCGTCC  | ATTCTTTTGA | TTATGACTGG | TACAATGTAT | CAGACCAGGC | AGATTTGAAG | 900  |
| AATCAGCTGG  | GAGATGCTGG | ATACGTATTA | TTTGGAGTGG | TGTTATTTGT | TTGGGAACTC | 960  |
| TTACCTACCA  | CCTTAGTCGT | TTATTTCTTC | CGAGTTAGAA | ATCCTACAAA | GGACCTTACC | 1020 |
| AACCCCTGGA  | TGGTCCCCAG | CCATGGATTG | AGTCCCAGAT | CTTATTTCTT | TGACAACCCT | 1080 |
| CGAAGATATG  | ACAGTGATGA | TGACCTTGCC | TGGAACATTG | CCCCTCAGGG | ACTTCAGGGA | 1140 |
| GGTTTTGCTC  | CAGATTACTA | TGATTGGGGA | CAACAACTA  | ACAGCTTCCT | GGCACAAGCA | 1200 |
| GGAACCTTGC  | AAAGACTCAA | CTTTGGATCC | TGACAAACCA | AGCCTTGGGT | AGCATCAGTT | 1260 |
| AACAGTTTTA  | TGGACGATTC | CTCAGATGAA | AAGCTTCAGA | AAAGCATAGT | GACAGCTGAA | 1320 |
| TTTTTTAGGGC | ACTTTTCCTT | AAGAAATAGA | ACTTGATTTT | TATTTGTTAC | AGGTTTCCAA | 1380 |
| TGGCCCCATA  | GGAATAAGCA | ATAATGTAGA | CTGATAAACC | CTTATTTTAG | TACTAAAGAG | 1440 |
| GGAGCCTTGC  | TATTTCACTG | GGTATAATTT | AAACTTTTTT | AAGAAAATCT | GTAATTTTAT | 1500 |
| AAAGATGTAT  | TTTGTATAAC | TTAAATAATA | ATGCTAAAGT | ATACTAGGGT | TTTTTTTTCT | 1560 |
| TGAGAATGTT  | ACTGCAATCA | TGTTGTAGTT | TGCACAGACT | TTTATGCATA | ATTCATTTTA | 1620 |
| AAAATATAGA  | ATATATGGTC | TAATAGTTTT | TTAAAGCTTT | TGGACTAAAG | TATTCACAA  | 1680 |
| ATCTTACCTC  | TTTAGGTCAC | TGATGGTCAC | TCCGATTCTG | AGTGCCACAT | TGGTAGACTC | 1740 |
| CTAAAATACA  | GTTGACAACT | TAGCCAATTG | CAACTCCAGT | GTTGATAATT | AAAATGAAAT | 1800 |
| GGTAAAGCAG  | CAGACTGTAA | GGTCTTTAGA | GATTTTTTTT | TTAAGGTTCA | GGCCGTAGGT | 1860 |
| TCCTCAAGGA  | ATCTCTTAAG | TTTTGCCCAA | AGACTGGTAC | TTCTTTTCAG | TAGGGCGCTA | 1920 |
| ATGTATACAC  | ATTAATGATA | AGTTGATAAC | ATTAAAAATG | TAGCTGACTT | ATCCTATTAA | 1980 |
| ACCTCCTCTG  | CTATGTTTAC | AGAACCCCCA | TAACCTTTTT | TCAGCCTAAT | GAAATCTAAT | 2040 |
| ATGCATTACC  | TCAGGGCCAC | ATCAAGAATA | CACCCCTTTC | CGAACTCACT | GAATGTTTCA | 2100 |
| TACATTTCAAG | GAGAAAATAA | GAGGGTCCAT | AAAGGGCATT | AATAACAAAT | ACCCCAAGCC | 2160 |
| GTTGAGCTAA  | GACTATGTGG | AATCCTAATA | GTTTTT     |            |            | 2196 |

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## (2) INFORMATION ON SEQ ID NO. 549:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 701 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

```

AATTAAAATA AATAGAAACA TACGGAGATT CTTTTATGTT GGATTTATTA TACCCTCCAC 60
CATTTTGGTC CCTGAAAAGG GAAAAGATAC ACGGTCGAGT AGTACAGGTA TGTGTTTCCC120
ACTACACATT ATGGCTATAA TGGAGTTGAA TTGCAAAACAG TAAAATTTTG TTTTGGATTG180

GTTTCCCCTG ATCCCCCAG ACAGGAGCTT CCTCTCCCAC CCTACCTGCC TGCCCTTAAG240
TTGTGTCCTA TTAAACTGGA CACAAATCTC ACCGGCTTTT AGTCTAATAA TTGAATCATA300
GCTACACACA GTGACACCAG AATAGCTACT TGTTTTTTTA TGTACCAGT GAGTAACTTG360
TTTATCCTTG TATGTAGAAA CTAATTTTCA CATGATCACA GATCTGTGTA ACATCTCTAG420
TTTGAATTTT CACACAATTT TAAAATGTCT ACTAGAAAAC TTACACCTTT TTGTTCCAAG480
GTGCTCTTCA TCTATAAAAC CGTGCGCATA CTTCAGTGTT CTTCTGAGGC CAAATTTTGT540
GGGTCGTGGG GGACAATTTT GTATTAACAT ACGTTATTTT GTAATTCATT CTCCAAATTT600
GAAGCTTTAT TAAAGGTATT CTATTTCCAC TGGCTTCCCT TAACTTGAAT AAAATTTACT660
CCCAGTGCCG TGGCTCATGC CTGCTGCAAT CCCAGCCCTT T 701

```

## (2) INFORMATION ON SEQ ID NO. 550:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2214 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

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## (vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

GCTAAAGAGG AGGATGCTAT ACTTTTCTAA ATGGCAAGAG ATGGGGAGAG AAGGGGATTA 60  
 AGAGTTGACC CGCAACCTCC CGGTGGATTC TTTGTTCTTA CCAGATCTCT TGGCCACTCC 120  
 CCTATTCTGA AGTCGTCTTG GCTCTCTTGA CTGCTCCCTT ATTCTGAAAGT CGTCTTGGCT 180  
 CTCTTGACTA CTCCCCTATT CTGAAGTCGT CTTGGCTCTC CTGACTACAC TATTTCAAGG 240  
 AATGATCACC AAGACACACA AAGTAGACCT TGGGCTCCCA GAGAAGAAAA AGAAGAAGAA 300  
 AGTGGTCAAA GAACCAGAGA CTCGATACTC AGTTTTAAAC AATGATGATT ACTTTGCTGA 360  
 TGTTTCTCCT TTAAGAGCTA CATCCCCCTC NTAAGAGTGT GGCCCATGGG CAGGCACCTG 420  
 AGATGCCTCT AGTGAAGAAA AAGAAGAAGA AAAAGAAGGG TGTCAGCACC CTTTGCGAGG 480  
 AGCATGTAGA ACCTGAGACC ACGCTGCCTG CTAGACGGAC AGAGAAGTCA CCCAGCCTCA 540  
 GGAAGCAGGT GTTTGGCCAC TTGGAGTTCC TCAGTGGGGA AAAGAAAAAN TAAGAAGTCA 600  
 CCTCTAGCCA TGTCCTGCTC CTCTGGGGTG AAAACCTCCC CAGNACCCNT AGACAGGGTG 660  
 AGGAGGAAAC CAGAGTTGGC AAGAAGCTCA AAAAANCACA AGAAGGAAAA AAAGGGGGNC 720  
 CCAGGACCCC ACNAGCCTTC TCGGTCCAGG ACCCTTGGTT CTGTGAGGCC AGGGAGGCCA 780  
 GGGATGTTGG GGACACTTGC TNCAGTGGGG AAGAAGGATG AGGAACAGGC AGCCTTGGGG 840  
 NCAGAAACGG AAGNCGGAAG AGCCCCAGAG AACACAATGG GAAGGTGAAG AAGAAAAAAA 900  
 AAATCCACCA GGAGGGAGAT GCCCTCCAG GCCACTCCAA GCCCTCCAGG TCCATGGAGA 960  
 GCAGCCCTAG GAAAGGAAGT AAAAAGAAGC CAGTCAAAGT TGAGGCTCCG GAATACATCC1020  
 CCATAAGTGA TGACCCTAAG TCCTCCGCAA AGAAAAAGAT GAAGTCCAAA AAGAAGGTAG1080  
 AGCAGCCAGT CATCGAGGAG CCAGCTCTGA AAAGGAAGAC GAGGAAGAAG AGGAAAGAGA1140  
 GTGGGGTAGC AGGAGACCCT TGGAGGGAGG AAACAGACAC GGACTTAGAG GTGGTGTGG1200  
 AAAAAAAGG CAACATGGAT GAGGCGACA TAGACCAGT GAGGCGAAAG GCCTTGCAAG1260  
 AAGAGATCGA TCGCGAGTCA GGCAAAACGG AAGCTTCTGA AACCAGGAAG TGGACGGGAA1320  
 CCCAGTTTGG CCAGTGGGAT ACTGCTGGTT TTGAGAACGA GGACCAAAAA CTGAAATTTTC1380  
 TCAGACTTAT GGGTGGCTTC AAAAACCTGT CCCCTTCGTT CAGCCGCCCC GCCAGCACGA1440  
 TTGCAAGGCC CAACATGGCC CTCGGCAAGA AGGCGGCTGA CAGCCTGCAG CAGAATCTGC1500  
 AGCGGGACTA CGACCGGGCC ATGAGCTTGG AAGTACAGCC GGGGAGCCGG CTTGCGGTGT1560  
 TCTCCACCGC CCCCACAAG ATCTTTTACA TTGACAGGAA CGCTTCCAAG TCAGTCAAGC1620  
 TGGAAGATTA AACTCTAGAG TTTTGTCCCC CCAAACTGC CACAATTGCT TTGATTATTC1680  
 CATTTATGCT GGAGATTACA AATTTTTTTT GGTGAACAAA TCAGATCTTG GTGAGGACCT1740  
 CGAGCAGTAA GATATAAATA ACTCCCNATA AGCTTAGNCG TTCCCAGTAA TGGAACACTA1800  
 GGCATAAANT GGTATTATTNC AGTTGTGCAA ATGAAAGCCA TCTGACAGTT GGCTNCACAT1860  
 TGAACACCTG TGGAGATTAA GGACGAGGAC AACTATATTG ATGGGCTTGG ATGAACTGGG1920  
 GCAGGGCAGC TCATATTTTCG GGAGCCAGGA GAACGAGTGA GTGCTAAAAC CTCCTGTTTT1980  
 CTGTGTTAAA CATTCCGTCC CTGTTTGAGA CATCAGTATG TACAGTTAAC TTTTGTTGAG2040  
 TGTTTAGCAG GTACTAGGGA CATACTAGTG TTTTCCTTAA TGTATTTAAT CTTCATAATT2100  
 ATGAAATGGG TGCTATTATT AGCCCCATCT TATAGATTAG GCAACTGAGG TTCAGGGATA2160  
 AAGTAATAAA ATTGCCTGGG GTCACCCAGC CACTAAAAAA AAAAAAAAAA AAAA 2214

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## (2) INFORMATION ON SEQ ID NO. 551:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

GCGCGGCCGG CGCCTGCGGG GCGAGAGGGT CGGGGCGAAG GGAAGCTAC GTCCCGGAGG 60  
 TGCGGTGTGG GGCACCGGGC GGGGCCGCGG GAACCGGCGC CCCACGGAGC TGCTGCTGTC 120  
 AGACCAACCC CGGGCCCCCA TCATCACTGC GCCGCGCTTT CAGGCGCCGA GAACTACCGT 180  
 TCCCGGCATG CCATGAAATT GGCCTCGGCG CTGAGGCGGG GTCCGGCCCT CCACCCGCTC 240  
 CCGCCGCGCG CGAATCGCGG TCGCGAGCCA TGGAGGAGGA GGCATCGTCC CCGGGGCTGG 300  
 GCTGCAGCAA GCCGCACCTG GAGAAGCTGA CCCTGGGCAT CACGCGCATC CTAGAATCTT 360  
 CCCCAGGTGT GACTGAGGTG ACCATCATAG AAAAGCCTCC TGCTGAACGT CATATGATTT 420  
 CTTCTTGGGA ACAAAGAAT AACTGTGTGA TGCCTGAAGA TGTGAAGAAC TTTTACCTGA 480  
 TGACCAATGG CTTCCACATG ACATGGAGTG TGAAGCTGGA TGAGCACATC ATTCCACTGG 540  
 GAAGCATGGC AATTAACAGC ATCTCAAAAC TGACTCAGCT CACCCAGTCT TCCATGTATT 600  
 CACTTCCTAA TGCACCCACT CTGGCAGACC TGGAGGACGA TACACATGAA GCCAGTGATG 660  
 ATCAGCCAGA GAAGCCTCAC TTTGACTCTC GCAGTGTGAT ATTTGAGCTG GATTTCATGCA 720  
 ATGGCAGTGG GAAAGTTTGC CTTGTCTACA AAAGTGGGAA ACCAGCATTA GCAGAAGACA 780  
 CTGAGATCTG GTTCTTGGAC AGAGCGTTAT ACTGGCATT TCTCACAGAC ACCTTTACTG 840  
 CCTATTACCG CCTGCTCATC ACCCACCTGG GCCTGCCCCA GTGGCAATAT GCCTTCACCA 900  
 GCTATGGCAT TAGCCACAG GCCAAGCAAT GGTTCAGCAT GTATAAACCT ATCACCTACA 960  
 ACACAAACCT GCTCACAGAA GAGACCGACT CCTTTGTGAA TAAGCTAGAT CCCAGCAAAG1020  
 TGTTTAAGAG CAAGAACAAG ATCGTAATCC CAAAAAAGAA AGGGCCTGTG CAGCCTGCAG1080  
 GTGGCCAGAA AGGGCCCTCA GGACCCTCCG GTCCCTCCAC TTCCTCCACT TCTAAATCCT1140  
 CCTCTGGCTC TGGAACCCC ACCCGGAAGT GAGCACCCCT CCCTCCAACCT CCCTACCAGC1200  
  
 TCCAGAGTGG TGGTTTCCAT GCACAGATGG CCCTAGGGGT GACCTCCAGT TTTGCGTGTG1260  
 GACCGTAGGC CTCTTTCTAG TTGAATGACC AAAATTGTAA GGCTTTTAGT CCCACCGACA1320  
 TTAGCCAGGC TCGTAGTGAG GCCTCCAGAG CAGGTTGTGC TGTCCTCTGC CTCTGGAAGC1380  
 AATGGGGAAT GTGGAATCAA GACAATGCCC AAAAAATTTT TAATGCAGCT GGTG 1434

002221 5622960

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| CCCGGAGAAG  | GTGGAGGGAG  | ACGAGAAGCC  | GCCGAGAGCC  | GACTACCCTC  | CGGGCCCAGT  | 60   |
| CTGTCTGTCC  | GTGGTGGATC  | TAAGCCTCAT  | CTGTATCCTC  | TTGTGATGGC  | GTGAAGGAAA  | 120  |
| GCCATGGCAG  | ATTTCCAGCC  | TGGTGATGCT  | GTACAGAACA  | CAGGTGGCCT  | GCTTCCATGC  | 180  |
| CTCCTCAGCT  | TCAAGAAACT  | AGAATGAACC  | GAAGCATTCC  | TGTGGAGGTT  | GATGAATCAG  | 240  |
| AACCATACCC  | AAGTCAGTTG  | CTGAAACCAA  | TCCCAGAATA  | TTCCCCGGAA  | GAGGAATCAG  | 300  |
| AACCACCTGC  | TCCAAATATA  | AGGAACATGG  | CACCCAACAG  | CTTGTCTGCA  | CCCACAATGC  | 360  |
| TTACAATTC   | CTCCGGAGAC  | TTTTCTCAAG  | CTCACTCAAC  | CCTGAAACTT  | GCAAAATCACC | 420  |
| AGCGCACTGT  | ATCCCGGCGAG | GTACCTGCC   | TGCGCACTCA  | AGTTCTGGAG  | GACAGTGAAG  | 480  |
| ACAGTTTTCTG | CAGGAGACAC  | CCAGGCGCTGG | GCAAAGCTTT  | CCTTTCTGGG  | TGCTCTGCAG  | 540  |
| TCAGCGAGCC  | TGCGTCTGAG  | TCTGTGGTTG  | GAGCCCTCCC  | TGCAGAGCAT  | CAGTTTTTCAT | 600  |
| TTATGGAAAA  | ACGTAATCAA  | TGGCTGGTAT  | CTCAGCTTTC  | AGCGGCTTCT  | CCTGACACTG  | 660  |
| GCCATGACTC  | AGACAAATCA  | GACCAAAGTT  | TACCTAATGC  | CTCAGCAGAC  | TCCTTGGGCG  | 720  |
| GTAGCCAGGA  | GATGGTGCAA  | CGGCCCCAGC  | CTNCACAGGA  | ACCGAGCAGG  | CCTGGATCTG  | 780  |
| CCAACCATAG  | ACACGGGATA  | TGATTCCCAG  | CCCCAGGATG  | TCCTGGGCAT  | CAGGCAGCTG  | 840  |
| GAAAGGCCCC  | TGNCCCTCAC  | CTCCGTGTGT  | TACCCCCAGG  | ACCTCCCCAG  | ACCTCTCAGG  | 900  |
| TCCAGGGAGT  | TCCCTCAGTT  | TGAACCTCAG  | AGGTATCCAG  | CATGTGCACA  | GATGCTGCCT  | 960  |
| CCCAATCTTT  | CCCCACATGC  | TCCATTGGAAC | TATCATTACC  | ATTGTCTCTGG | AAGTCCCGAT  | 1020 |
| CACCAGGTGC  | NCATATGGCC  | ATGACTACCC  | TCGAGCAGCC  | TACCAGCAAG  | TGATCCAGCC  | 1080 |
| GGCTCTGCCT  | GGGNCAGCCC  | CTNNGCCTGG  | AGCCAGTGTG  | AGAGGCCTGC  | ACCCTGTGCA  | 1140 |
| GAANNGGTTA  | TCCTGAATTA  | TCCCAGCCCC  | TGGGACCAAG  | AAGAGAGGCC  | CGCACAGAGA  | 1200 |
| GACTGCTCCT  | TTCCGGGGCT  | TCCAAGGCAC  | CAGGACCAGC  | CACATCACCA  | GCCACCTAAT  | 1260 |
| AGAGCTGGTG  | CTCCTGGGGA  | GTCTTGGGAG  | TGCCCTGCAG  | AGCTGAGACC  | ACAGGTTCCC  | 1320 |
| CAGCCTCCGT  | CCCCAGCTGC  | TGTGCCTAGA  | CCCCCTAGCA  | ACCCTCCAGC  | CAGAGGAACT  | 1380 |
| CTAAAAACAA  | GCAATTTGCC  | AGAAGAATTG  | CGGAAAGTCT  | TTATCACTTA  | TTCGATGGAC  | 1440 |
| ACAGCTATGG  | AGGTGGTGAA  | ATTCGTGAAC  | TTTTTGTGTTG | TAAATGGCTT  | CCAAACTGCA  | 1500 |
| ATTGANCANT  | ATTTGAGGAT  | AGAATCCGAG  | GCATTGATAT  | CATTNAAATG  | GATGGAGCGC  | 1560 |
| TACCTTANGG  | GATAAGACCG  | TGATGATAAT  | CGTAGCAATC  | AGCCCCNAA   | NTACAAANNC  | 1620 |
| AGGACGTNGG  | NAAAGNCGCT  | GANGTCNGCA  | GCTGGACGAG  | GATGAGCATG  | GCTTACATAC  | 1680 |
| TAAGTACATT  | CATCGAATGA  | TGCAGATTGA  | GTTCATAAAA  | CAAGGAAGCA  | TGAATTTTCAG | 1740 |
| ATTCATCCCT  | GTGCTCTTCC  | CAAATGCTAA  | GAAGGAGCAT  | GTGCCACCT   | GGCTTCAGAA  | 1800 |
| CACNTCATGT  | CTACAGCTGG  | CCCAAGAATN  | AAAAAAAACA  | TCCTGCTGCG  | GCTGCTNGAG  | 1860 |
| AGAGGAAGAG  | TATGTGGCTC  | CTCCACGGGG  | GCCTCTGCCC  | ACCNCTTCAG  | GTGGTTCCCT  | 1920 |
| TGTGANCAAC  | GTTTCATCCCC | AGATCACTGA  | GGCCNAGGCC  | ATGTTTGGGN  | GCCTTGTTCT  | 1980 |
| GNACAGCATT  | CTGGCTGAGG  | CTNNGTCGGT  | AGCANNCTCC  | TGGCTGGTTT  | TTNTTCTGTT  | 2040 |
| CCNTCCCCGA  | NGAAGCCCTC  | TGGNNCCCCC  | ANGGAAACCT  | GTTGTGCAGA  | GCTCTTCCCC  | 2100 |
| GGAGACCTCC  | NACACANCCC  | TGGNCTTTGA  | AGTGGAGTCT  | GTGNACTGNC  | TCTGCATTNC  | 2160 |
| TCTGCTTTTN  | AAAAAAACCA  | TTGCAGGTGN  | CCAGTGTCCC  | ATATGTTNCC  | TCCTNGACAG  | 2220 |
| NTTTGTATGTN | GTNCCATTCT  | NGGGCCTCTC  | AGTGCTTAGC  | AAGTAGATAA  | TGTAAGGGAT  | 2280 |
| GTNGGCAGCA  | AATGGAAATG  | ACTACAAACA  | CTCTCCTATC  | AATCACTTCA  | GGCTACTTTT  | 2340 |
| ATGAGTTAGC  | CAGATGCTTG  | TGTATCCTCA  | NGACCAAAC   | GATTCATGTA  | CAAATAATAA  | 2400 |
| AATGTTTACT  | CTTTTGTAAA  | AAAAAAAAAA  | AAAA        |             |             | 2434 |

## (2) INFORMATION ON SEQ ID NO. 554:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1457 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

ACTAACCCAG AGTTGTGGCA TTATTAATTA TCACTGGTCT TCTTAATCGT AAAACGGGGG 60  
 ACCCCAGAGG CAAGGAAATT TCCATTACCC TATATTGGGC TTAAACTTAA AGGAGTATAT 120  
 CCACTATCAA GAGCTTAGTA CAAAGGCTGG GGTGAAGTTA CATTATACCT GGGCGTTTTA 180  
 CCATACCAGG GACCCACCT CAACAATGAC TGTGGAAGAC CAAAGGAGAT ACCTAGGTTT 240  
 AGATTATAAT AAATCACCCA GCACCACCTG AATGTATTAT CCACAAAGAT ATAGCAATAA 300  
 TAAAGTTTAT ATATACATAT ATTTATCTTG GTAACCTGAG GGCTAAAAAC GTGGAATACG 360  
 ATAATTCTTC TCAAGAGGTC CATCTGTAAG AAAGGGACCC AAAAGGACAG TGTTTGTGTT 420  
 GCATAAAATA TGGGTAAAGT GGAGTTGGGA ACAAAGGGTG GTTCTCTTAG CTCTTCCAC 480  
 ATCTCTCTTT GATAAGGACT GAAACCCTGT TGATTCATGA TAAACGTTTC CTTTTTTTTT 540  
 TTTTTTGGCA GCGGGGAGAG GGAAAGAGGA GGAAATGGGG TTTGAGGACC ATGGCTTACC 600  
 TTTCTGCTT TTAGCCCATC ACACCCCATT TCCTCCTCTT TCCCTCTCCC CGCTGCCAAA 660  
 AAAAAAAAAA AGGAAACGTT TATCATGAAT CAACAGGGTT TCAGTCCTTA TCAAAGAGAG 720  
 ATGTGGAAAG AGCTAAAGAA ACCACCCTTT GTTCCCAACT CCACTTTACC CATATTTTAT 780  
 GCAACACAAA CACTGTCCTT TTGGGTCCCT TTCTTACAGA TGGACCTCTT GAGAAGAATT 840  
 ATCGTATTCC ACGTTTTTAT CCCTCAGGTT ACCAAGATAA ATATATGTAT ATATAACCTT 900  
 TATTATTGCT ATATCTTTGT GGATAATACA TTCAGGTGGT GCTGGGTGAT TTATTATAAT 960  
 CTGAACCTAG GTATATCCTT TGGTCTTCCA CAGTCATGTT GAGGTGGGCT CCCTGGTATG 1020  
 GTAAAAAGCC AGGTATAATG TAACTTCACC CCAGCCTTTG TACTAAGCTC TTGATAGTGG 1080  
 ATATACTCTT TTAAGTTTAT CCCCAATATA GGGTAATGGA AATTTCTCTG CCTCTGGGTT 1140  
 CCCCATTTTT ACTATTAAGA AGACCAGTGA TAATTTAATA ATGCCACCAA CTCTGGCTTA 1200  
 GTTAAGTGAG AGTGTGAAC GTGTGGCAAG AGAGCCTCAC ACCTCACTAG GTGCAGAGAG 1260  
 CCCAGGCCTT ATGTTAAAAT CATGCACTTG AAAAGCAAAC CTTAATCTGC AAAGACAGCA 1320  
 GCAAGCATT TACGGTCATC TTGAATGATC CCTTTGAAAG TTTTGTGTTG GTTGGTTTGG 1380  
 TTTAAATCA AGCCTGAGGC TGGGTGGAAA CAGGTAGCCT ACACACCCCA AATTGGGGGT 1440  
 GGTCCCGGGG GAATGTT 1457

00673395.122700

## (2) INFORMATION ON SEQ ID NO. 555:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 741 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

CCTCCTAAAA GACTGGGAAA GCAGCTTTGG GCTTTGGGTC CTCCTAAAAA AACCAAGGCG 60  
 GATGACTTGG GGTTTGGATC CCCTTCGGAT GTCACTCGAA AAAGCCTTAG CAGACCTGAT120  
 TGAGAAGGAA CTGTCCCGTT CAAAGACCAA CCTTCCCTTT CGCCCCACAT CTCTTCAGAA180  
 CTCCTCTTCA CACACTACAA CCGCCAAAGG TCCCAGGCTC TGGATTCCCTG CATCCTGCTG240  
 CAGCTACAAA TGCCAATTCT CTAAATAGTA CCTTTTCAGT CTTGCCCCAG AGGTTCCCTC300  
 AATTTTCAGCA GCACCGAGCG GTTTATAATT CATTTCAGTTT TCCAGGCCAG GCAGCCCGCT360  
 ATCCTTGGAT GGCCTTTCCA NCGCAATAGC ATCATGCNAC TTGAACCACA CAGCAAACCC420  
 CACCTCAAAT AGTAATTTCT TGGACTTGAA TCTCCCGCCA CAGCACAACA CAGGTCTGGG480  
 AGGGATCCCT GTAGCAGGGG AAGAAGAGGT GAAGGTTTCG ACCATGCCAC TGTC AACCTC540  
 TTCCCATTC A TTACAACAAG GACAGCAGCC TACAAGTCTC CACACTACTG TGGCCTGACA600  
 ACAGAACTGA GAGGAGAGGA TTAGACTCTG GGGTGCTTGC ATGGGCAACT GGATTTTTTGC660  
 ATGATTCCCTT TATGATTTTG CTTTAAATGT ATACACCCAG AAGAGCCAAT ATAAACGTTTC720  
 CTCATGCCTA AAAAAAAAAA A 741

## (2) INFORMATION ON SEQ ID NO. 561:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 470 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

007221"56E2960

## (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

TDQPNIQSVK IHSPLRNPN KGCECPRRD GGFIFKCVDR DVRMEFFHSE ILDGNQLHIA 60  
 DEVEFTVVPD MLSAQRNHAI RIKKLPGKTV SFHSHSDHRF LGTVEKEATF SNPKTTSPPNK120  
 GKEKEAEDGI IAYDDCGVKL TIAFQAKDVE GSTSPQIGDK VEFISIDKQR PGQQVATCVR180  
 LLGRNSNSKR LLGYVATLKD NFGFIETANH DKEIFFHYSE FSGDVDSLEL GDMVEYSLSK240  
 GKGNKVSARK VNKTHSVNGI TEEADPTIYS GKVIRPLRSV DPTQTEYQGM IEIVEEGDMK300  
 GEVYPFGIVG MANKGDCLQK GESVKFQLCV LGQNAQTMAV NITPLRRATV ECVKDQFGFI360  
 NYEVGDSKKL FFHVKEVQDG IELQAGDEVE FSVILNQRTG KCSACNVWRV CEGPKAVAAP420  
 RPDRLVNRLK NITLDDASAP RLMVLRQPRG PDNSMGFGAE RKIRQAGVID 470

## (2) INFORMATION ON SEQ ID NO. 562:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 126 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

LNAILNFFHM EKELLAISYF IVNEAKLIFH TFHCGPAQGC DVVSHSLCIL AQDTQLELDA 60  
 LPFLQAIPFV GHPNDKAWID LTFHIALLHN LNHSVLVSLC WINTPQGANY FARVNGGISF120  
 LSNAIH 126

## (2) INFORMATION ON SEQ ID NO. 563:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 85 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

KSHTSCNLLS RPLFVTNTKF NLISYLRSSR SFHILGLKSN SQFHPTVIIS NNAILSLLLF60  
 AFIWASGFRI GKSGFFFYRA QKTVI 85

007227 563395 122700



## (2) INFORMATION ON SEQ ID NO. 564:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 549 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

LYPNFLVNEL ILKQKQRFEE KRFKLDHSVS STNGHRWQIF QDWLGTDDQN LDLANVNLML 60  
 ELLVQKKKQL EAESHAAQLQ ILMEFLKVAR RNKREQLEQI QKELSVLEED IKRVEEMSG120  
 YSPVSEDSTV PQFEAPSPSH SSIIDSTEYS QPPGFSGSSQ TKKQPWYNST LASRRKRLTA180  
 HFEDLEQCYF STRMSRISDD SRTASQLDEF QECLSKFTRY NSVRPLATLS YASDLYNGSS240  
 IVSSIEFDRD CDYFAIAGVT KKIKVYEYDT VIQDAVDIHY PENEMTCNSK ISCISWSSSYH300  
 KNLLASSDYE GTVILWDGFT GQRSKVYQEH EKRCWSVDFN LMDPKLLASG SDDAKVKLWS360  
 TNLDNSVASI EAKANVCCVK FSPSSRYHLA FGCADHCVHY YDLRNTKQPI MVFKGHRKAV420  
 SYAKFVSGEE IVSASTDSQL KLWNVGKPYC LRSFKGHINE KNFVGLASNG DYIACGSENN480  
 SLYLYYKGLS KTLTTFKFDT VKSVLDKDRK EDDTNEFVSA VCWRALPDGE SNVLIAANSQ540  
 GTIKVLELV 549

## (2) INFORMATION ON SEQ ID NO. 565:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 132 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

TLYFVYIDMC NSQRGWEIRT LQIIHCYIIV HICYFVTFVF SFVFFFFFFF FFCGSINFYC 60  
 FVIYFYSKEF VLSQKLDNT TKSSNVHGVV LMVESWLGIP NVPKVIKEGK EKKKKIFKTN120  
 PKPMMTLGRD IT 132

## (2) INFORMATION ON SEQ ID NO. 566:

- (i) SEQUENCE CHARACTERISTIC:

002221"565/960

- (A) LENGTH: 90 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

GTVLSSLTGE YKPLISSTLL ISSSKTLSSF WICSSCSLLF LLATLRNSIR ICSWAACDSA60  
SSCFFECTSN SNIRLTAKS RLSWSVPNQS 90

(2) INFORMATION ON SEQ ID NO. 567:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 331 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

SANHKLEVNG TDGLAPVEVE ELLRQASERN SKSPTEYHEP VYANPFYRPT TPQRETVTPG 60  
PNFQERIKIK TNGLGIGVNE SIHNMGNGLS EERGNNFNHI SPIPPVPHPR SVIQQAEK120  
HTPQKRLMTP WEESNVMQDK DAPSPKRLS PRETIFGKSE HQNSSPTCQE DEEDVRYNIV180  
HSLPPDINDT EPVTMIFMGY QQAEDSEEDK KFLTGYDGII HAELVVIDDE EEEDEGEAEK240  
PSYHPIAPHS QVYQPAKPTP LPRKRSEASP HENTNHKSPH KNSISLKEQE ESLGSPVHHS300  
PFDAQTTGDG TEDPSLTALR MRMAKLGKKV I 331

(2) INFORMATION ON SEQ ID NO. 568:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 216 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

00673395.122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

LSLTSRMEEA ELVKGRQLQAI TDKRKIQEEI SQKRLKIEED KLKHQHLKKK ALREKWLLDG 60  
ISSGKEQEEM KKQNOQDOHQ IQVLEQSILR LEKEIQDLEK AELQISTKEE AILKKLKSIE120  
RTTEDIIRSV KVEREERAE SIEDIYANIP DLPKSYIPSR LRKEINEEKE DDEQNRKALY180  
AMEIKVEKDL KTGESTVLSS NTSGHQMTLK GTGVKV 216

(2) INFORMATION ON SEQ ID NO. 569:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 132 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

LEKLHICFPQ LFGNFSQIMT TTYSHGLIWY TVMIIFWTSE KINKISRREI CKCFLVSSSK 60  
DVIYIGGTTLR SPFFPALPFS SLKLLRMDPQ SHLQLSEHQM GNGGQGCLSF LLALSEIWNF120  
CGGIYDLCFH ED 132

(2) INFORMATION ON SEQ ID NO. 570:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 199 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

NEVTPWSFWW WTKLTFFFPL ALKKSSRVSS SHLPRIYQAF LMSATFNEDV QALKELILHN 60  
PVTCLKLQESQ LPGPDQLQQF QVVCETEEDK FLLLYALLKL SLIRGKSLLF VNTLERSYRL120  
RLFLEQFSIP TCVLNGELPL RSRCHIISQF NQGFYDCVIA TDAEVLGAPR QRAMRPRRRA180  
KTGTMASRFL ERTVVALGH 199

09673395 122700

## (2) INFORMATION ON SEQ ID NO. 571:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 195 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

QVRRAALLSS AMEDSEALGF EHMGLDPRLL QAVTDLGWSR PTLIQEKAIP LALEGKDLLA 60  
RARTGSGKTA AYAIPMLQLL LHRKATGPVV EQAVRGLVLV PTKELARQAQ SMIQQLATYC120  
ARDVRVANVS AAEDSVSQRA VLMEKPDVVV GTPSRILSHL QQDSLKLKRD LELLVVDEAD180  
LLFSFGFEEE LKSL 195

## (2) INFORMATION ON SEQ ID NO. 572:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 76 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

DIGHSDIPST VGSQLLNHGL CLPCQLLGRN KNKASHCLFY HRTCRLPMEQ QLQHRNSISG60  
RLPGARAGPS QEVLPF 76

## (2) INFORMATION ON SEQ ID NO. 573:

- (i) SEQUENCE CHARACTERISTIC:

09673395-122700

- (A) LENGTH: 91 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

DSQVGRGPQR NSSLHTGRSV HWGEATGSLR HLQWGDAQPL LFLGGKLRFK LPGGKSMGRK60  
QALXLLRVSV SPFFPLCLIN KFHFSPNS L 91

(2) INFORMATION ON SEQ ID NO. 574:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 89 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

EKWNLLIRHK GKKGETETLS KXRACFLPMD FPPGSLNRSF PPRKRRGWAL PHWRWRKLPV60  
ASPQCTLLPV CRLEFLWGPL PTWLSHCPL 89

(2) INFORMATION ON SEQ ID NO. 575:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

09673395 "122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

LIRCLRLFSL HVMERKLSTS FLRLPATQLL IHIWSEPWYP STIHARKLDV YSLPFFPLFG60  
 DFLSSAEDG VLVCPMATKI 80

## (2) INFORMATION ON SEQ ID NO. 577:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

LLPLLLLLLIH GDTPXGPGPX XQEQAPNHRH GLEEXRISXK SCMGXVDWNG PEGVEIYVDG 60  
 KEPHNKSQSS QLGFKTNGHX KSSEXVXHVDV LDNRKEAGVK VKEGHEHQNQ QDPASELHVL120  
 FGGALTHGGD ARKHALPFRT GFSRSTQQPP PRARFLPLCR T 161

## (2) INFORMATION ON SEQ ID NO. 578:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 160 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

QTDNLSEERQP XGKXVCRGCP QGECSWERAV LLXPGRPALS XTLLXKXAPC EVNWVXVRGS 60  
 XXCXGAPAXT EXPXQRXAAS AXAGLEXSXA XAGXAGCCCX GLPXVWSXLA LPTASLEASX120  
 XPRPAASPRT SCPSTLPQAT KTRVLPNKX XLGTXSCLIF 160

0067395.12200

## (2) INFORMATION ON SEQ ID NO. 579:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 437 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

SQGVLSDDGV WRVKSIPNGK GSSPLPTATT PKPLIPTEAS IRVWGTSCTS HLHPRSICMI 60  
 QKYNHDGEAG RLEAFSQGES VLKEPKYQEE LEDRLHFYVE ECDYLQGFQI LCDLHDGFGSG120  
 VGAKAAELLQ DEYSGRGIIT WGLLPGPYHR GEAQRNIYRL LNTAFGLVHL TAHSSLVCPL180  
 SLGGSGLLRP EPPVSFPYLH YDATHLPFHCS AILATALDTV TVPYRLCSSP VSMVHLADML240  
 SFCGKKVVTG GAIIPFPLAP GQSLPDSLMO FGGATPWTPL SACGEPSTGR CFAQSVVLRG300  
 YRQSMHPKPO NQRDTSTLCP SCMYHWGRNL GSVFTTAAAW SHEFFPSAAD SLQGGSSSLPP360  
 PLLKLQSTGY GSGWFPPQGR SSVLSLSPQQ WRASQCLGHC VPLRPCTRPW KPWPETSPNS420  
 TCGAGPASWM LEWSTMT 437

## (2) INFORMATION ON SEQ ID NO. 580:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 277 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

TERLLLDGPP PHSPETPQFP PTTGAVLYTV KRNQVGPEVR SCPKASPRLO KEREQKAVS 60  
 ESEALMLVWD ASETKLPPT VEPPASFLSP VSSKTRDAGR RHVSGKPDQ ERWLPSSRAR120  
 VKTRDRTCPV HESPSGIDTS ETSPKAPRGG LAKDSGTQAK GPEGEQQPKA AEATVCANNS180  
 KVSSTGEKVV LWTREADRVI LTMCEQGAQ PQTFNIISSQ LGNKTPAEVS HRFRELMQLF240  
 HTACEASSED EDDATSTNSA DQLSDHGDLL SEEELDE 277

## (2) INFORMATION ON SEQ ID NO. 581:

00673395.122700

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 172 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

FPESHSSSSS SDRRSPWSDS WSALLVLVAS SSSSELASQA VWKSCMSSRK RWETSAGVLF 60  
 PSCWEMMLKV CGCAPCSWHM VRITRSASLV HRTTFSPVEL TLLLLAHTVA SAAFGCCSPS120  
 GPLACVPLSL AKPPLGALGE VSEVSIPDGD SWTGHVLSLV FTLALLEGSH LS 172

(2) INFORMATION ON SEQ ID NO. 582:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 549 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

EFPPGLTEPT AVRALARARR TRAGSASDPE RSPGAMALSE LALVRWLQES RRSRKLILFI 60  
 VFLALLLDNM LLTVVVPIIP SYLYSIKHEK NATEIQTARP VHTASISDSF QSIFSYDENS120  
 TMVTGNATRD LTLHQTATQH MVTNASAVPS DCPSEDKDLL NENVQVGLLF ASKATVQLIT180  
 NPFIGLLTNR IGYPIPIFAG FCIMFVSTIM FAFSSSYAFL LIARSLQGIG SSCSSVAGMG240  
 MLASVYTDDE ERGNVMGIAL GGLAMGVLVG PFGSVLYEF VGKTAPFLVL AALVLLDGAI300  
 QLFVLQPSRV QPESQKGTPL TTLLKDPYIL IAAGSISFAN MGIAMLEPAL PIWMMETMCS360  
 RKWQLGVAFL PASISYLGIT NIFGILAHKM GRWLCALLGM IIVGVSLICI PFPKNIYGLI420  
 APNFGVGFAN GMVDSSMMPI MGYLVDLRHV SVYGSVYAIA DVAFCMGYAI GPSAGGAIAK480  
 AIGFPWLMTI IGIIDILFAP LCFFLRSPPA KEEKMAILMD HNCPIKTKMY TQNNIQSYPI540  
 GEDEESES D 549

(2) INFORMATION ON SEQ ID NO. 583:

- (i) SEQUENCE CHARACTERISTIC:

09673395 "122700



- (A) LENGTH: 121 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

YLLSHWNQYF WDTCTQNGEV ALCSSGNDNC WSQHFMYSIS KKHLWTHSSE LWSWFCKWNG 60  
GFVNDAYHGL PRRPAARVRL WECVRHCGCG ILYGVCYRSF CWWCYCKGNW ISMAHDNYWD120  
N 121

(2) INFORMATION ON SEQ ID NO. 584:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 106 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

DGGSVHWPFGR LDFCSILLML NAVQITWDDG DHDSEQHVVO QQRQEHDEQD ELPRAAALLQ 60  
PADQRQLAQG HGSGAPLGVA CAACPGPPCP RQRPHRSLR QSGREF 106

(2) INFORMATION ON SEQ ID NO. 585:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 409 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

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|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| KSRLSVTLMP  | VQLSEHPewn | ESMHSRLISV | GGLPVLASMT | KAADPRFRPR | WKVILTFVVG | 60  |
| AAILWLLCSH  | RPAPGRPPTH | NAHNWRLGQA | PANWYNDTYP | LSPPQRTPag | IRYRIAVIAD | 120 |
| LDTEPTAQDE  | NTWRSDLKKG | YLTLSDSGDK | VAVEWDKDHG | VLESHLAEKG | RGMELSDLIV | 180 |
| FNGKLYSVDD  | RTGVVYQIEG | SKAVPWVILS | DGDGTVEKGF | KAEWLAVKDE | RLYVGGLGKE | 240 |
| WTTTTGDVVN  | ENPEWVKVVG | YKGSVDHENW | VSNYNALRAA | AGIQPPANLI | HESACWSDTL | 300 |
| QRWFFLPERR  | SQERYSEKDD | ERKGANLLLS | ASPDGDIADV | SHVGAVVPTH | GFSSFKFIPN | 360 |
| TDDQIIIVALK | SEEDSGRVAS | YIMAFTLDGR | FLLPETKIGS | VKYEGVEEII |            | 400 |

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 249 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| KLSPDGLAQC | FRFELNELDA | FVFHASDLGL | RQQEAPVQRE | GHDVGGDSAA | VLLGFEGHND | 60  |
| LVVGVGDELE | GREAVSGDHR | PDVAHSDVAE | VRGGAQQQVG | ALALVVLAV  | ALLAGAARQE | 120 |
| EPALQRVTPA | GRLMDEVSWR | LDAGSSPQGV | VVGHPVLVVH | AALVAHHLHP | LRVLVHHITR | 180 |
| SGRPLLAQAA | HVQTLVLHCQ | PFGLEAFLHG | AVAVGQNHFG | HGFAAFDLVD | DPRPVIHGEV | 240 |
| FPIENNOVG  |            |            |            |            |            | 249 |

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 157 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

LEFFIPCLGS VNEACLFPGV SFHGLYFSSS SGSFAGSSLW KLHERWLGLG FAGVYSRVKA 60  
EWDLRPRLTG TQAEKGRFHH SQCPPHSNYL TPTPTLTPTP PRDRQGCHGG PEGAGSGCPC120  
AGPSOTSPPL KLKHSCEEGS EEGPLSHGCL FPPLCHR 157

## (2) INFORMATION ON SEQ ID NO. 588:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 144 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

NTMAVAAVKW VMSKRTILKH LFPVQNGALY CVCHKSTYSP LPDDYNCNVE LALTS DGRTI 60  
VCYHPSVDIP YEHTKPIPRP DPVHNNEETH DQVLKTRLEE KVEHLEEGPM IEQLSKMFFT120  
TKHRWYPHGR YHRCRKNLNP PKDR 144

## (2) INFORMATION ON SEQ ID NO. 589:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 128 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

IHQTAFSQMA NEAHFSLIPP GTSASSVFWR IQILTTVIP SMRIPTVLSS KEHFAKLFYH 60  
RSFLKVENFF FQSGFQHLIM CFFIIMHRIW PRDRFCVFIW NVHRRVVAYY CPAIRSQSKL120  
YVAIIVIW 128

## (2) INFORMATION ON SEQ ID NO. 590:

- (i) SEQUENCE CHARACTERISTIC:

00673395 12200

- (A) LENGTH: 61 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

KLVCLEADSK SSFSSEHLFS YHLISILKHH GCSCSKMGDV KENYLETFIS SPKWSFILCL60  
S 61

(2) INFORMATION ON SEQ ID NO. 591:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 173 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

AQESPWQLCR GARTSKRKLP KLGMEQHCNE MCPSSLFLP GAYKAQMYSD VWTNTKKKKK 60  
KKKKKAFLSH RHKTQIIYCY EALFTNGQFL HFIAACERLP DGRPISLVLQ TSSQAAFYQK120  
GENSCLSFLK NAFLYLSIRH YTSELYKRP G TMSLVDTFH CSVAPFLAWE ASA 173

(2) INFORMATION ON SEQ ID NO. 592:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 105 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60  
 RDLALLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

## (2) INFORMATION ON SEQ ID NO. 593:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 105 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60  
 RDLALLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

## (2) INFORMATION ON SEQ ID NO. 594:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 172 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

TPALRARS LR DRCARAPCPH GGQRRRRRL NAEGAEGARG GGSSYSEMAE TVADTRRLIT 60  
 KPQNLNDAYG PPSNFLEIDV SNPQTVGVGR GRFTTYEIRV KTNLPPIFKLK ESTVRRRYSD120  
 FEWLRSELER ESKVVVPPLP GKAFRLRQFL EEMMEYLMTI LLRKENKGWS SL 172

## (2) INFORMATION ON SEQ ID NO. 595:

00227 5667960

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 127 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

SAAGCQPRSP PFRSCCRRR GLPPPPPSA AAAGAAARRG DTGLARSGRE ENEHVERAFT 60  
 PHAKLLPAPL KLPPSPGGEK RLTSWNATPG SREARPLGR GTADWGVRRS GVMGLGVANR120  
 FRPDYSA 127

(2) INFORMATION ON SEQ ID NO. 596:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 123 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

FTSQPFKVTV SSSNSRFFQL ENRKICLDPD FVSGEAAPAD PHRLRVAHID LEEVAGGSVG 60  
 VIQVLRRLGDQ PPGVSHGLRH FAVAAAAAAG SLRPLRVQPP PPALLPAVGT RGSRAAVAKR120  
 TST 123

(2) INFORMATION ON SEQ ID NO. 597:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 262 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

(2) INFORMATION ON SEQ ID NO. 598:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

(2) INFORMATION ON SEQ ID NO. 599:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

AEDTIQKRNS QFETVTPPAP NCGDEERKQW LWFLSEGRLR TERSNHQGHR FWKSSRGGWL60  
EEQ 63

## (2) INFORMATION ON SEQ ID NO. 600:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 336 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

KLNFNTMRCC HICKLPGRVM GIRVLRSLV VILVLLLVAG ALTALLPSVK EDKMLMLRRE 60  
 IKSQ GKSTMD SFTLIMQTYN RTDLLLKL LN HYQAVPNLHK VIVVWNNIGE KAPDELWNSL120  
 GPHPIPVIFK QQTANRMRNR LQVFPELETN AVLMVDDDTL ISTPDLVFAF SVWQQFPDQI180  
 VGFVPRKHVS TSSGIYSYGS FEMQAPGSGN GDQYSMVLIG ASFFNSKYLE LFQRQPAAVH240  
 ALIDDTQNCD DIAMNFIIAK HIGKTSGIFV KPVNMDNLEK ETNSGYSGMW HRAEHALQRS300  
 YCINKLVNIY DSMPLRYSNI MISQFGFPYA NYKRKI 336

## (2) INFORMATION ON SEQ ID NO. 601:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 101 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

HALKILQHYD FPVWFSCQL QKKNIKVKQT KTNLKTAWHL SSFSMLCIFL SNIMNFIYSR 60  
 SLYNRKKS AV LLGYKIHITF ESQEVGLIQL GLLMKSFHPG I 101

## (2) INFORMATION ON SEQ ID NO. 602:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 90 amino acids  
 (B) TYPE: Protein

002221 5557960



(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

FKSFNKRSVL LYVCIMRVKE SMVDLPWDFI SLRNMSILSS LTLGSKAVKA PATSNNTMT60  
TKDNRSTRIP ITLPGSLQMW QHLIVLKFNF 90

(2) INFORMATION ON SEQ ID NO. 603:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 163 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

IYGVSFLLFN IKNIYVSVIP CQGCLLVCLR FCFIFIHVVV IFSSQFLLVS PFPGSFLLLL 60  
LSVGDDKLVS LRALHLWIFL XSLTGQPAPV GSGPVLRLPR SLFHLQVCLP XPAPGLAPAA120  
ACPSEALLSP PGSHGWFPIS QLVSLNPKPL RNWGLVSGTC CYQ 163

(2) INFORMATION ON SEQ ID NO. 604:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 150 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00/227" 56EE/960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

PLSFLMYKTL LSGLEFEHLW XFIYFAXVCG QSNIFPKYIL PRKXKKQIRX FDXKXNRPKK 60  
 GAXTWSRAWX RGKAXRGQVC CGQICAYFIT GVKXKQXSID VXRIYTVXRN XRXFXKNNRN120  
 ) TXWXXFYHXX YTFSLWXNXL TKLXFKIKLM 150

## (2) INFORMATION ON SEQ ID NO. 605:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 108 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

LDFKXQFCES IXPQAKCVXX MIKXXPXXIP VFLKXVPXIS XHCIYPXDIN XTLFSFYSSN 60  
 KVGTDLSTTN LPSXCLASXP CSAPGXXPLX XPVXFVKXP NLLLAFSW 108

## (2) INFORMATION ON SEQ ID NO. 606:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 203 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

GPSALVHSVR PDLCSNPLSC GSLACMAYTG ELGLWAVQTQ GSHFAFPLLS PFSILALRQN 60  
 FSQRRTLCCP RSAVILPFLP SFHPSSAQMK SSRNSSFLPL WDSETGNLQG GVFPSPFLFL120  
 STPRGTAAV PTSGTELHTI VGKLQGPLL VLAHL CYWS FWQKRKMIEP RVAPECSSLT180  
 VEGPKLVFRA HPRREVIRCH AFC 203

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## (2) INFORMATION ON SEQ ID NO. 607:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 154 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

EVROKEWCLL WSFPFPGAGL CAKLGPQHIW STLLVGARPE HLTQPVHTAP RVPPLSQAGP 60  
 TAPGSADKGM ACPLRCQNSI QKAPPQVDVV PGAGEESGTT TLAVNLSNRG LGFLVAASCP120  
 GLEVHRSRGV PLGTKDMPHW GCNGEKSGKL GAQL 154

## (2) INFORMATION ON SEQ ID NO. 608:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

CGVLSLRWVQ QPWFLWGLRI RIVGREKLLL EDFLSQSPRE VERRNFCWTS SGQRKDG MKV 60  
 EKAELQLSGD NKEFFSGKSF VLEQGWMGT TKEKQSVTLG FGQPRGPAPQ YKPYRPGTHR120  
 RVD 123

## (2) INFORMATION ON SEQ ID NO. 609:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 88 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

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(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

LVEPNGLFWF HFSASRRQNK ESHSKMFIVD NMSLKVVPLC SYSTEEMIHI PIIDMVSQSE60  
ESFRRLLHKYV LCTCPMLGNR KIIVIDKT 88

(2) INFORMATION ON SEQ ID NO. 610:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 80 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

SCFHKLSTQE PDGKKNKNYA DNYRKINPNL VKLVKACTFQ RFIRTGLNRE FLLNKMALTL60  
VPRNWNQPORS YTGDNLSALIL 80

(2) INFORMATION ON SEQ ID NO. 611:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 71 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

MGITHECVIL LGASANSLTV VPSLTLPVHH LRRLDPSLTS PFLKPVSFSL LPNWLWLFLQ60  
PFHSRAIFAK E 71

(2) INFORMATION ON SEQ ID NO. 612:

(i) SEQUENCE CHARACTERISTIC:

002221 56552960

- (A) LENGTH: 395 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

APMRPERPRP RGSAPGPMET PPWDPARNDS LPPTLTPAVP PYVKLGLTVV YTVFYALLFV 60  
 FIYVQLWLVL RYRHKRLSYQ SVFLFLCLFW ASLRTVLFSF YFKDFVAANS LSPFVFWLLY120  
 CFPVCLQFFT LTLMNLYFTQ VIFKAKSKYS PELLKYRLPL YLASLFISLV FLLVNLTCV180  
 LVKTGNWERK VIVSVRVAIN DTLFVLCVAVS LSICLYKISK MSLANIYLES KGSSVCQVTA240  
 IGVTVILLYT SRACYNLFIL SFSQNKSVHS FDYDWINVSD QADLKNQLGD AGYVLFVVL300  
 FVWELLPTTL VVYFFVRNP TKDLTNPGMV PSHGFSPRSY FFDNPRRYDS DDDLAWNIAP360  
 QGLQGGFAPD YYDWGQQTNS FLAQAGTLQR LNFGS 395

(2) INFORMATION ON SEQ ID NO. 613:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 213 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

ARCAETPAGA AAVSPDEAR ASPAARQRPR PDGDPAVGPS PQRLAAAHAD PGRAPLREAW 60  
 PHRRHLRVLR AALRVHLRAA LAGAALPPQA AQLPERLPLS LPLLGLPADR PLLLLLQRLR120  
 GGQFAQPLRL LAALLPCVP AVFHPhADEL VLHAGDFQSQ VKIFSRTIQI PVAPLPGLPL180  
 HQPCFPVGEF NLCCAGKDGK LGEEGYRLCA SGH 213

(2) INFORMATION ON SEQ ID NO. 614:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

LGFENHLREV QVHQREGKEL QAHREAVEQP EDEGAERIGR HEVFEVEGEE DGPQGGPEEA 60  
EKEEDALVAE PLVAVTQHQP ELHVDEHEEQ RVEHGVDGGE AKLHVGGHGR GQRGRQRVVA120  
GWVPRRGLHR AGGAAARPPT LGPHRGSRPP PPRGSPRIA P 161

(2) INFORMATION ON SEQ ID NO. 615:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 102 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

HKKTSSYSGV TVCSYDSIIR LKAGEICVQF NRTQLKGRQV GWERKLLSGG IRGNQSKTKF 60  
YCLQFNSIIA IMCSGKHIPV LLDRVSFPFS GTKMVEGIIN PT 102

(2) INFORMATION ON SEQ ID NO. 616:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 86 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

VTCLSLYVET NFTMITDLN ISSLNFTIL KCLLENLHLF VPRCSSSIKP WAYFSVLLRP60  
NEVGRGGQFC INIRYFVIHS PNLKLY 86

00673395.122700

## (2) INFORMATION ON SEQ ID NO. 617:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 76 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

RMLIQNCPPR PTKFGLRRTL KYAHGFIDEE HLGTKRCKFS SRHFKIVWKF KLEMLHRSVI60  
 MVKLVSTYKD KQVTHW 76

## (2) INFORMATION ON SEQ ID NO. 618:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 378 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

SRCRFCCRLS AAFLPRAMLG LAIVLAGRLN EGDRLFPPPI SLRNFSFWSS FSKPAVSHWP 60  
 NWVPVHFLVS EASVLPDSRS ISSCKAFRLT WSMCASSMLP FFSNTTSKSV SVSSLQGSPA120  
 TPLSFLFFLV FLFRAGSSMT GCSTFFLDFI FFFAEDLGSS LMGMYSGAST LTGFFLLPFL180  
 GLLSMDLEGL EWPGRASPSW WIFFFFFFFFP LCSLGLFRLP FLXPRLPVPH PSSPLXQVSP240  
 TSLASLASQN QGSWTEKAXG VLGPPFFPSC XFLSFLPTLV SSSPCLXVLG RFSPQRHGTW300  
 LEVTSXFFFS PLRNSKWPNL CFLRLGDFSV RLAGSVVSGS TCSSQRVLTP FFFFFFFFTR360  
 GISGACPWAT LLXGGCSS 378

## (2) INFORMATION ON SEQ ID NO. 619:

- (i) SEQUENCE CHARACTERISTIC:

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- (A) LENGTH: 269 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

GTGSLGXRNG XRKSPREHNG KVKKKKKIHQ EGDALPGHSK PSRSMESSPR KGSKKKPVKV 60  
 EAPEYIPISD DPKSSAKKKM KSKKKVEQPV IEEPALKRKT RKKRKESGVA GDPWREETDT120  
 DLEVVLEKKG NMDEAHIDQV RRKALQEEID RESGKTEASE TRKWTGTQFG QWDTAGFENE180  
 DQKLKFLRLM GGFKNLSPSF SRPASTIARP NMALGKKAAD SLQQNLQRDY DRAMSLEVQP240  
 GSRLAVFSTA PNKIFYIDRN ASKSVKLED 269

(2) INFORMATION ON SEQ ID NO. 620:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 218 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

VRVCFLPPRV SCYPTLFFLL PRLPFQSWLL DDWLLYLLFG LHLFLCGGLR VITYGDVFRS 60  
 LNFDWLLFTS FPRAALHGPG GLGVAWEGIS LLVDFFFLH LPIVFSGALP XSVSXPKAAC120  
 SSSFFPTXAS VPNIPLGLPL TEPRVLDREG XWGPGXPFFS FLXFFELLAN SGFLLTLSXG180  
 XGEVFTPEAW DMARGDFLXF LFPTEELQVA KHLLEAG 218

(2) INFORMATION ON SEQ ID NO. 621:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 389 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

AAGACGARGS GRRGSYVPEV RCGAPGGAAG TGAPRSCCCQ TNP GPPSSLR RAFRRRELPF 60  
 PACHEIGLGA EAGSGPPPAP AARESRSRAM EEEASSPGLG CSKPHLEKLT LGITRILESS120  
 PGVTEVTIIE KPPAERHMIS SWEQKNNCVM PEDVKNFYLM TNGFHTWSV KLDEHIIPLG180  
 SMAINSISKL TOLTQSSMYS LPNAPTLADL EDDTHEASDD QPEKPHFDSR SVIFELDSCN240  
 GSGKVCLVYK SGKPALAEDT EIWFDRALY WHFLDTFTTA YYRLLITHLG LPQWQYAFTS300  
 YGISPQAKQW FSKYKPITYN TNLLTEETDS FVNKLDPSKV FKSKNKIVIP KKKGPVQPAG360  
 GQKGPSGPSG PSTSSTSKSS SGSGNPTRK 389

(2) INFORMATION ON SEQ ID NO. 622:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 109 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

ARPAPAGREG RGEGEATSRR CGVGHRAGPR EPAPHGAAV RPTPGPHHHC AALSGAENYR 60  
 SRHAMKLASA LRRGPALHPL PPRANRGREP WRRRHRPRGW AAASRTWRS 109

(2) INFORMATION ON SEQ ID NO. 623:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 96 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

007227 5657960

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

RSAGGFSSMMV TSVTPGEDSR MRVMFVVSFS RCGLLQPSPG DDASSSMARD RDSRAAGAGG60  
GDPASAPRP ISWHAGNGSS RRLKARRSDD GGPGLV 96

(2) INFORMATION ON SEQ ID NO. 624:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 218 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

CCTEHRWPAS MPPQLQETRM NRSIPVEVDE SEPYPSQLLK PIPEYSPEEE SEPPAPNIRN 60  
MAPNSLSAPT MLHNSSGDFS QAHSTLKLAN HQRPVSRQVT CLRTQVLEDS EDSFCRRHPG120  
LGKAFPSGCS AVSEPAESV VGALPAEHQF SFMEKRNQWL VSQLSAASPD TGHDSKSDQ180  
SLPNASADSL GGSQEMVQRP QPXQEPSRPG SANHRHGI 218

(2) INFORMATION ON SEQ ID NO. 625:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 212 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

0022700 "56E/960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

NLQITSGLYP GRSPACALKE WRTVKTVSAG DTQAWAKLSL LGALQSASLR LSLWLEPSLQ 60  
 SISFHLWKNV INGWYLSFQR LLLTLAMTQT NQTKVYLMPQ QTPWAVARRW CNGPSLHRNR120  
 AGLDLPTIDT GYDSQPQDVL GIRQLERPLX LTSVCYPQDL PRPLRSREFP QFEPQRYPAC180  
 AQMLPPNLSP HAPWNYHYHC PGSPDHQVXI WP 212

## (2) INFORMATION ON SEQ ID NO. 630:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 184 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

FMINVSFFFF LAAGRGKEEE MGCDGSKAGK VSHGPQTPFP PLSLSPLPKK KKKETFIMNQ 60  
 QGFSPYQREM WKELKKPPFV PNSTLPIFYA TQTLSEWVPF LQMDLLRRII VFHVFSPOVT120  
 KINICIYNLY YCYIFVDNTE RWCWVIYYNL NLGISFGLPQ SLLRWGPWYG KTPRYNVTSP180  
 QPLY 184

## (2) INFORMATION ON SEQ ID NO. 631:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 138 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

GPWLTFFAFD PSHPISSSFP LPAAKKKKKE TFIMNQOGFS PYQREMWKEL KKPPFVPNST 60  
 LPIFYATQTL SFWVPFLQMD LLRRIIVFHV FSPQVTKINI CIYNLYCYI FVDNTRWCW120  
 VIYYNLNLGI SFGLPQSC 138

002221 5688 960

## (2) INFORMATION ON SEQ ID NO. 632:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

WVKGRKGKGPW SSNPISSSFP LPAAKKKKKG NVYHESTGFQ SLSKRDVERA KETTLCSQLH60  
 FTHILCNTNT VLLGPFLTDG PLEKNYRIPR F 91

## (2) INFORMATION ON SEQ ID NO. 633:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

RNHAKIQLPM QAPQSLILSS QFCCQATVVW RLVGCCPCCN EWEEVDSGMV ETFTSSSPAT 60  
 GIPPRPVLCC GGRFKSKLL FEVGFAVWFK XHDAIAXERP SKDSGLPGLE N 111

## (2) INFORMATION ON SEQ ID NO. 634:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

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(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

) LRRNCPVQRP TFPFAPHLFR TPLHTLQPPK VPGSGFLHPA AATNANSLNS TFSVLPQRFP60  
QFQQHRAVYN SFSFPGQAAR YPWMAFPXQ 89

(2) INFORMATION ON SEQ ID NO. 635:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 89 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

FIQFSRPGSP LSLDGLSXAI ASCXLNHTAN PTSNSNFLDL NLPPQHNTGL GGIPVAGEEEE60  
VKVSTMPLST SSHSLQQGQQ PTSLHTTVA 89

002221-56667960